

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:48:38 ; Search time 77.2888 Seconds  
(without alignments)  
1089.410 Million cell updates/sec

Title: US-09-852-797-76  
Perfect score: 1521  
Sequence: 1 MARSRRLRLLLRLYLWA.....SSKATTSNDFXHKTSFII 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1518	99.8	298	2	AAW85457 Secreted
2	1518	99.8	298	4	AAU00512 Human jun
3	1518	99.8	298	5	ADP61801 Human pol
4	1518	99.8	298	6	ABR58532 Human vas
5	1517	99.7	298	2	AAW75220 Human sec
6	1517	99.7	298	5	AAE26983 Human gen
7	1517	99.7	298	5	AAE27121 Human gen
8	1517	99.7	298	6	ABR47926 Human sec
9	1517	99.7	298	6	ABR00172 Human gen
10	1517	99.7	298	6	ABU64994 Human sec
11	1517	99.7	298	7	ABE91670 Human sec
12	1517	99.7	298	7	ADC74331 Human sec
13	1514	99.5	298	6	AAO16452 Human sec
14	1502.5	98.8	303	4	AAW23693 Human EST
15	1465	96.3	312	2	AAV23324 A33 relat
16	1465	96.3	312	2	AAV08060 Human PRO
17	1465	96.3	312	2	AAV13354 Amino aci
18	1465	96.3	312	3	AAV33421 Human PRO
19	1465	96.3	312	3	AAV70668 Human PRO
20	1465	96.3	312	3	AAV24401 Human PRO
21	1465	96.3	312	3	ADC78384 Human PRO
22	1465	96.3	312	4	ABR80222 Human PRO
23	1465	96.3	312	4	AAU08821 Human imm
24	1465	96.3	312	4	AAU12339 Human PRO
25	1465	96.3	312	4	AAV53081 Human ang

26	1465	96.3	312	6	ABU71600 Human PRO
27	1465	96.3	312	6	ABO17783 Novel hum
28	1465	96.3	312	6	ABU71455 Human PRO
29	1465	96.3	312	6	ABU81037 Human PRO
30	1465	96.3	312	6	ABU71901 Human sec
31	1465	96.3	312	6	ABO01784 Novel hum
32	1465	96.3	312	6	ABU66737 Human PRO
33	1465	96.3	312	6	ABU54357 Human sec
34	1465	96.3	312	6	ABO47372 Human sec
35	1465	96.3	312	6	ABU59818 Novel sec
36	1465	96.3	312	6	ABO25008 Human sec
37	1465	96.3	312	6	ABU64509 Human sec
38	1465	96.3	312	6	ABU67355 Human sec
39	1465	96.3	312	6	ABO14875 Human sec
40	1465	96.3	312	6	ABU07738 Human A-3
41	1465	96.3	312	6	ABU67013 Human sec
42	1465	96.3	312	6	ABU69632 Novel hum
43	1465	96.3	312	6	ABO14814 Human sec
44	1465	96.3	312	6	ADA45855 Novel hum
45	1465	96.3	312	6	ADA76286 Human PRO

## ALIGNMENTS

RESULT 1  
AAW85457  
ID AAW85457 standard; protein; 298 AA.  
XX  
AC AAW85457;  
XX  
DT 25-FEB-1999 (first entry)  
XX  
DE Secreted protein encoded by clone ct864\_4.

Secreted protein; nutritional activity; immune stimulating; vaccine;  
suppressing activity; haematopoiesis regulating activity;  
tissue growth activity; activin; inhibin activity; chemotactaxis;  
chemokinetic activity; haemostasis; thrombolytic activity; receptor;  
ligand; anti-inflammatory; cadherin; tumour invasion suppressor;  
tumour inhibition; gene therapy.

Homo sapiens.  
WO9842739-A2.  
01-OCT-1998.

20-MAR-1998; 98WO-US005653.  
21-MAR-1997; 97US-00822167.  
19-MAR-1998; 98US-00044466.

(GEMY ) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
Spaulding V, Agostino MJ;  
WPI; 1998-609890/51.  
N-PSDB; AAV82780.

New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA libraries.

Claim 17; Page 73-74; 113pp; English.

The present sequence represents a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating

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CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity (no data is
CC given in the specification to support these activities). The
CC polynucleotide is also stated to be useful for gene therapy
XX
SQ Sequence 298 AA;
Query Match 99.8%; Score 1518; DB 2; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.1e-117;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLLLRYLVVVALGYHKA YGFSAPKQQVVTAYVQEQAILACKTPKKTYSR 60
DB 1 MARRSRHRLLLLLRYLVVVALGYHKA YGFSAPKQQVVTAYVQEQAILACKTPKKTYSR 60
QY 61 LEWKILGRSVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQQN 120
DB 61 LEWKILGRSVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSTYTNKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
DB 181 LGSQSTNSSTYTNKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
QY 241 IAAVVVVALVTSVCGLVGYCAQRKGYSKETSFKQSNSSSKATTMSSEDFKHTKSFII 298
DB 241 IAAVVVVALVTSVCGLVGYCAQRKGYSKETSFKQSNSSSKATTMSSEDFKHTKSFII 298
RESULT 2
AAU00512
ID AAU00512 standard; protein; 298 AA.
AC AAU00512;
XX
DT 09-MAY-2001 (first entry)
XX
DE Human junctional adhesion protein (JAM2).
XX
KW Junctional adhesion protein; JAM2; cellular localisation;
KW cellular expression; immunoprecipitation; stroke; phosphorylation;
KW glycosylation; paracellular migration; inflammatory disease; arthritis;
KW asthma; rheumatoid arthritis; inflammatory bowel disease;
KW Crohn's disease.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..28 "Possible signal peptide #2"
FT Peptide 1..20 "Possible signal peptide #1"
FT Protein 21..298 "Possible mature JAM2 #1"
FT Protein 29..298 "Possible mature JAM2 #2"
FT Domain 237..254 "Transmembrane domain"
XX
XX WO200114404-A1.
PN
XX 01-MAR-2001.
XX
XX 23-AUG-2000; 2000WO-US023158.
XX
XX 24-AUG-1999; 99US-0150459P.
XX
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
PA
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XX
PI Cunningham S, Trindad Arrate Barros M;
XX WPI; 2001-218425/22.
XX N-PSDB; AAS00512.
XX
PT Novel nucleic acids encoding human junctional adhesion protein useful for
PT producing antibodies that are suitable for therapeutic purposes.
XX
XX Claim 4; Page 46-47; 51pp; English.
XX
XX The sequence represents a human junctional adhesion molecule 2 (JAM2).
XX The polynucleotide encoding the polypeptide is useful for recombinant
XX production of JAM-2 protein, which in turn is useful for the production
XX of antibodies. The antibodies may be used for probing cellular
XX localisation and/or expression of JAM2 in tissues under normal and
XX disease states, for immunoprecipitating JAM2 protein from cells and/or
XX stroke tissues to determine whether it is modified by glycosylation and
XX phosphorylation, and for determining JAM2 function. The antibodies
XX inhibit interaction of JAM2 with inflammatory cells or influences their
XX paracellular migration, and is therefore useful for alleviating
XX inflammatory diseases such as arthritis, asthma, rheumatoid arthritis,
XX inflammatory bowel disease and Crohn's disease
XX
SQ Sequence 298 AA;
Query Match 99.8%; Score 1518; DB 4; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.1e-117;
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARRSRHRLLLLLRYLVVVALGYHKA YGFSAPKQQVVTAYVQEQAILACKTPKKTYSR 60
DB 1 MARRSRHRLLLLLRYLVVVALGYHKA YGFSAPKQQVVTAYVQEQAILACKTPKKTYSR 60
QY 61 LEWKILGRSVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQQN 120
DB 61 LEWKILGRSVSFVYVYQQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQQN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSTYTNKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
DB 181 LGSQSTNSSTYTNKTGTLOFNTVSKLDTGEYSCARNVGYRCPGKRMQVDDLNSGI 240
QY 241 IAAVVVVALVTSVCGLVGYCAQRKGYSKETSFKQSNSSSKATTMSSEDFKHTKSFII 298
DB 241 IAAVVVVALVTSVCGLVGYCAQRKGYSKETSFKQSNSSSKATTMSSEDFKHTKSFII 298
RESULT 3
ABP61801
ID ABP61801 standard; protein; 298 AA.
XX
XX AC ABP61801;
XX
XX DT 04-OCT-2002 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 155.
XX
XX KW Human; cytostatic; antirheumatic; antiarthritic; vulnary; analgesic;
XX antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
XX neuroprotective; nootropic; osteopathic; haemostatic; vasotrophic;
XX antitumor; fungicide; antidiabetic; antisthmatic; antiallergic;
XX immunostimulant; antiparasitic; secreted protein; transmembrane protein;
XX stem cell; growth factor; nervous system disease; neuropathy;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX osteoporosis; severe combined immunodeficiency; SCID; infection;
XX multiple sclerosis; rheumatoid arthritis; gene therapy.
XX
XX OS Homo sapiens.
```

[illegible]

CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
 CC drug screening, particularly for identifying agents for treating these  
 CC pathologies  
 XX  
 SQ Sequence 298 AA;

Query Match 99.8%; Score 1518; DB 6; Length 298;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-117;  
 Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVYQEAAILACKTPKKTVXSR 60  
 DB 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120  
 DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180  
 DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLINSIGI 240  
 DB 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLINSIGI 240

QY 241 IAAVVVVALVIVSVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 DB 241 IAAVVVVALVIVSVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298

RESULT 5  
 AAW75220  
 ID AAW75220 standard; protein; 298 AA.  
 AC AAW75220;  
 XX  
 DT 29-JAN-1999 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 25 clone HTEEB42.  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Key  
 FT Misc-difference 42 /label= unknown  
 FT  
 FT Misc-difference 58  
 FT  
 FT Misc-difference 58 /label= unknown  
 XX  
 FN WO9840483-A2.  
 XX  
 XX  
 PD 17-SEP-1998.  
 XX  
 XX 12-MAR-1998; 98WO-US004858.  
 XX  
 PR 14-MAR-1997; 97US-0040710P.  
 PR 14-MAR-1997; 97US-0040762P.  
 PR 30-MAY-1997; 97US-0048100P.  
 PR 30-MAY-1997; 97US-0048189P.  
 PR 30-MAY-1997; 97US-0048357P.  
 PR 30-MAY-1997; 97US-0050934P.  
 PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.  
 PR 19-DEC-1997; 97US-0068368P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;  
 PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;  
 PI Ferrie AM;  
 XX  
 XX WPI; 1998-520811/44.  
 DR N-PSDB; AAV34310.  
 XX  
 XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to  
 PT develop products for the diagnosis and treatment of e.g. inflammation,  
 PT cancers, CNS disorders or immune system disorders.  
 XX  
 PS Claim 1; Page 168-169; 201pp; English.  
 XX  
 CC This sequence represents a secreted human protein encoded by the gene  
 CC clone detailed in the descriptor line. The gene can be used to generate  
 CC fusion proteins by linking to the gene to a human immunoglobulin FC  
 CC portion (e.g. AAV34277) for increasing the stability of the fused protein  
 CC as compared to the human protein only. The invention relates to 28 novel  
 CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino  
 CC acid sequences AAW75196-W75235) which are useful for preventing, treating  
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,  
 CC pathological conditions can be diagnosed by determining the amount of the  
 CC new polypeptides in a sample or by determining the presence of mutations  
 CC in the new polynucleotides. Specific uses are described for each of the  
 CC 28 polynucleotides, based on which tissues they are most highly expressed  
 CC in (see AAV34286 for described uses)  
 XX  
 SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 2; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVYQEAAILACKTPKKTVXSR 60  
 DB 1 MARRSRHRLLLRLVVALGYHKAYGFSAPKDDQOVVAVYQEAAILACKTPKKTVXSR 60

QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120  
 DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180  
 DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLINSIGI 240  
 DB 181 LGSQSTNSSYTWTGTGLQFNVTSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLINSIGI 240

QY 241 IAAVVVVALVIVSVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 DB 241 IAAVVVVALVIVSVCGLGVCYAOBKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298

RESULT 6  
 AAE26983  
 ID AAE26983 standard; protein; 298 AA.  
 XX  
 AC AAE26983;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 XX Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO.76.  
 DE  
 KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;  
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;  
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;  
 KW



inflammatory bowel disease; neurodegenerative disorder; hepatitis;  
Parkinson's disease; Alzheimer's disease; cardiovascular disorder;  
atherosclerosis; myocarditis; renal disorder; fungicide; virucide;  
hyperproliferative disorder; acute glomerulonephritis; tonsillitis;  
respiratory disorder; rhinitis; sinusitis; neurological disease;  
endocrine disorder; Addison's disease; reproductive system disorder;  
endometriosis; vasotropic; vulnerable; cytostatic; nootropic; cardiant;  
anti-HIV; tranquiliser; gout; antiparasitic.  
Homo sapiens.  
Key Location/Qualifiers  
Peptide 1..22 /label= Signal\_peptide  
Protein 23..298 /label= "Human mature secreted protein"  
Misc-difference 42 /label= Unknown  
Misc-difference 58 /note= "Encoded by GWG"  
Misc-difference 59 /label= Unknown  
Misc-difference 60 /note= "Encoded by TSC"  
US200207287-A1.  
20-JUN-2002.  
11-MAY-2001; 2001US-00852659.  
11-SEP-1998; 98US-00152060.  
(RUBE/) RUBEN S M.  
(ROSE/) ROSEN C A.  
(LIYI/) LI Y.  
(ZENG/) ZENG Z.  
(KYAW/) KYAW H.  
(FISC/) FISCHER C L.  
(LIH/) LI H.  
(SOPP/) SOPPET D R.  
(GENT/) GENTZ R L.  
(WEIY/) WEI Y.  
(MOOR/) MOORE P A.  
(YOUN/) YOUNG P E.  
(GREE/) GREENE J M.  
(FERE/) FERRIE A M.  
Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;  
Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;  
Ferrie AM;  
WPI: 2002-598780/64.  
N-PSDB: AAD44660.  
Novel human secreted polypeptides and polynucleotides for diagnosing,  
preventing, treating immune, hyperproliferative, cardiovascular,  
neurological, reproductive disorders and identifying modulators of  
therapeutic use.  
Claim 11; Page 186; 209pp; English.  
AAB44636-AAD44676 represent cDNAs corresponding to 28 human secreted  
protein genes, and AAE26959-AAE26999 represent the proteins they encode.  
AAE27000-AAE27025 represent human secreted protein fragments or their  
variants. The secreted proteins and genes are useful for preventing,  
treating or ameliorating medical conditions, e.g., by protein or gene  
therapy. Specific uses are described for each of the 28 genes, based on  
the tissues in which they are most highly expressed and include  
developing products for the diagnosis or treatment of immunodeficiencies,  
e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe  
combined immunodeficiencies, autoimmune disorders e.g., systemic lupus  
erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune  
thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,  
Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions

including septic shock, sepsis, reperfusion injury, inflammatory bowel  
disease, Crohn's disease, haematopoietic disorders, respiratory disorders  
e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory  
bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and  
breast), central nervous system (CNS) disorders e.g., ischaemic brain  
injury and/or stroke, neurodegenerative disorders e.g., Parkinson's  
disease and Alzheimer's disease, AIDS-related dementia and prion disease,  
cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,  
inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,  
sarcoidosis and allogeneic transplant rejection, blood-related disorder  
(thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative  
disorders, respiratory disorders e.g., rhinitis, sinusitis, tonsillitis,  
lung cancer, allergic disorders, pneumonitis, renal disorders e.g., acute  
glomerulonephritis, neurological diseases, liver disorders, endocrine  
disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,  
infectious diseases and reproductive system disorders e.g., endometriosis.  
The present sequence represents a human secreted protein of the invention  
Sequence 298 AA;  
Query Match 99.7%; Score 1517; DB 5; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARRSRHLLLLRLVVALGCHYKAYGFSAPDQVVTAVYQEAAILACKTPKTVXR 50  
DB 1 MARRSRHLLLLRLVVALGCHYKAYGFSAPDQVVTAVYQEAAILACKTPKTVXR 50  
QY 61 LEWKILGRSVFVYQQTLOGDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
DB 61 LEWKILGRSVFVYQQTLOGDFKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
QY 121 LEEDVTLEVLVAPVPSCEVFSALSGTVVBLRQDKEGNPAPETWFKDGLLENPR 180  
DB 121 LEEDVTLEVLVAPVPSCEVFSALSGTVVBLRQDKEGNPAPETWFKDGLLENPR 180  
QY 181 LGSQSTNSSTYTNMTKTGTLOFNTVSKLDTGEVSCARNVGVYRCPGKMQVDDLNISGI 240  
DB 181 LGSQSTNSSTYTNMTKTGTLOFNTVSKLDTGEVSCARNVGVYRCPGKMQVDDLNISGI 240  
QY 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFKQSNSSSKATTSENDFKTKGFII 298  
DB 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFKQSNSSSKATTSENDFKTKGFII 298  
RESULT 7  
AAE27121  
ID AAE27121 standard; protein; 298 AA.  
XX  
AC AAE27121;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Human gene 25 encoded secreted protein HTEB542, SEQ ID NO:76.  
XX  
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;  
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;  
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;  
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;  
KW infection; corneal infection; skin aging; food additive; preservative;  
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;  
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;  
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;  
KW vulnerable.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..22 /label= Signal\_peptide  
FT Protein 23..298 /note= "Mature human secreted protein"  
FT Misc-difference 42

FT /label= Unknown  
 FT /note= "Encoded by GWG"  
 FT Misc-difference 58  
 FT /label= Unknown  
 FT /note= "Encoded by TSC"  
 XX  
 PN US2002076756-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00853161.

XX 02-FEB-2001; 2001US-0265583P.

PA (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYV/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIEH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEI/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREB/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI: 2002-574454/51.

DR N-PSDB; AAD44878.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful  
 PT for diagnosing, preventing, treating or ameliorating medical conditions  
 PT and as food additives or preservatives.

XX Claim 11; Page 186-187; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted  
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.  
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Secreted protein sequences of the invention are useful for the  
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.  
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of  
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,  
 CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous  
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,  
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The  
 CC polypeptides can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues and in chemotaxis. They can also be used as food  
 CC additives or preservative to increase or decrease storage capabilities,  
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors  
 CC and other nutritional components. The present sequence represents a human  
 CC secreted protein of the invention

XX Sequence 298 AA;

SQ Query Match

Best Local Similarity 99.7%; Score 1517; DB 5; Length 298;

Matches 298; Conservativity 100.0%; Pred. No. 1.3e-117;

Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLLLLYLVVALGYHKAYGFSAPKQOOVTVAXYQEAIIACKTPKTYXSR 60

DB 1 MARRSRHRLLLLLLYLVVALGYHKAYGFSAPKQOOVTVAXYQEAIIACKTPKTYXSR 60

QY 61 LEWKKLGRSVSVFYVYQOITLQGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
 DB 61 LEWKKLGRSVSVFYVYQOITLQGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
 QY 121 LEEDTIVTLEVLVAPAVPSCEVPSSSALSGTVVELRQDKEGNAPEYTFKDGIRLLENPR 180  
 DB 121 LEEDTIVTLEVLVAPAVPSCEVPSSSALSGTVVELRQDKEGNAPEYTFKDGIRLLENPR 180  
 QY 181 LGSQSTNSSYTNKTTGTLQFNVTSKLDTGEVSCBARNVGYRRCPGKRMQVDDNLNLSGI 240  
 DB 181 LGSQSTNSSYTNKTTGTLQFNVTSKLDTGEVSCBARNVGYRRCPGKRMQVDDNLNLSGI 240  
 QY 241 IAAVWVVALVIVSGGLGVCYAQKRGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 DB 241 IAAVWVVALVIVSGGLGVCYAQKRGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298

RESULT 8

ABR47926

ID ABR47926 standard; protein; 298 AA.

XX ABR47926;

XX 12-JUN-2003 (first entry)

XX Human secreted protein, SEQ ID 817.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

XX vulnerary; antiinflammatory; nootropic; neuroprotective;

XX antiparkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

XX WC200295010-A2.

XX 28-NOV-2002.

XX 19-MAR-2002; 2002WO-US009785.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-129429/12.

XX Novel human secreted proteins, useful for detecting, preventing,

XX diagnosing, prognosticating, treating and/or ameliorating cardiovascular

XX disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 817; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47633-  
 CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins  
 CC and their coding sequences are useful for the preparation of a diagnostic  
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular  
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,  
 CC proliferative disorders and/or cancerous diseases and conditions, for  
 CC wound healing and epithelial cell proliferation, to treat inflammation or  
 CC infection, for treating thrombosis and arteriosclerosis, for treating or  
 CC preventing neural damage which occurs in neuronal disorders or  
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
 CC disease, to enhance bone and periodontal regeneration and aid in tissue  
 CC transplants or bone grafts, to prevent skin aging or hair loss, to  
 CC stimulate growth and differentiation of haematopoietic cells and bone  
 CC marrow cells when used in combination with other cytokines, to maintain  
 CC organs before transplantation or for supporting cell culture of primary

CC tissues, to increase or decrease differentiation or proliferation of  
CC embryonic stem cells, or to modulate mammalian characteristics or  
CC metabolism. Note: The sequence data for this patent was published in  
CC electronic format and is available from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 6; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARRSRRLRLRLRLRLVVALGYHKAAGFAPKDDQVTVAVYQEAAILACKTPKTVASR 60  
Db 1 MARRSRRLRLRLRLRLVVALGYHKAAGFAPKDDQVTVAVYQEAAILACKTPKTVASR 60

Qy 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
Db 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120

Qy 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVLRQDKEGNPAPEYTWFKDGRLLLENPR 180  
Db 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVLRQDKEGNPAPEYTWFKDGRLLLENPR 180

Qy 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNVSVYRRCPCGRMVDLNLISGI 240  
Db 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNVSVYRRCPCGRMVDLNLISGI 240

Qy 241 IAAVVVALVISVCGLVCAQKGYFSEKTSFQKSNSSSKATTMSNDPKHTKSFII 298  
Db 241 IAAVVVALVISVCGLVCAQKGYFSEKTSFQKSNSSSKATTMSNDPKHTKSFII 298

RESULT 9  
ABR00172  
ID ABR00172 standard; protein; 298 AA.

XX AC ABR00172;  
XX AC ABR00172;  
XX DT 03-APR-2003 (first entry)  
XX DE Human gene 152 encoded secreted protein HTEB42, SEQ ID NO:461.

XX KW Human; secreted protein; digestive disorder; gastrointestinal disorder;  
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;  
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;  
KW immune disorder; inflammation; infection; wound healing; drug screening;  
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;  
KW antiinflammatory; immunosuppressive; vulnary; chromosome 21q21.2.

XX OS Homo sapiens.  
XX FN WO200276488-A1.  
XX PD 03-OCT-2002.  
XX PF 19-MAR-2002; 2002WO-US008276.  
XX PR 21-MAR-2001; 2001US-0277340P.  
XX PR 19-JUL-2001; 2001US-0306171P.  
XX PR 13-NOV-2001; 2001US-0331287P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM;  
XX DR WPI; 2003-029900/02.  
XX DR N-PSDB; ABZ71351.  
XX PT New human secreted proteins and nucleic acids, useful for detecting,  
PT preventing, diagnosing, prognosticating, treating and/or ameliorating  
PT e.g. gastrointestinal diseases and disorders, or cancers.

PS  
XX  
CC ABZ71150-ABZ71478 represent cDNAs corresponding to 178 human secreted  
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.  
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The  
CC invention also encompasses antibodies specific for the secreted proteins,  
CC the use of the secreted proteins in drug screening, and recombinant  
CC vectors and host cells comprising a nucleic acid of the invention. The  
CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
CC fragments specific for the secreted proteins, and modulators of protein  
CC activity are useful for diagnosing, treating, ameliorating or preventing  
CC digestive disorders. Such conditions include disorders of the mouth,  
CC oesophagus, stomach, small intestine, large intestine, liver, biliary  
CC tract and pancreas, and include cancers of these organs and tissues. The  
CC secreted proteins and their nucleic acids may also be used in the  
CC treatment of immune disorders, inflammation, infection,  
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids  
CC of the invention may be used for chromosome identification, chromosome  
CC mapping, in gene therapy, for identifying individuals from minute  
CC biological samples, as hybridisation probes, and as molecular weight  
CC markers. The present sequence represents a human secreted protein of the  
CC invention  
XX  
SQ Sequence 298 AA;

Query Match 99.7%; Score 1517; DB 6; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARRSRRLRLRLRLVVALGYHKAAGFAPKDDQVTVAVYQEAAILACKTPKTVASR 60  
Db 1 MARRSRRLRLRLRLVVALGYHKAAGFAPKDDQVTVAVYQEAAILACKTPKTVASR 60

Qy 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120  
Db 61 LEWKILGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQGN 120

Qy 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVLRQDKEGNPAPEYTWFKDGRLLLENPR 180  
Db 121 LEEDTVTLVLVAPVPSCVPSSALSGTVVLRQDKEGNPAPEYTWFKDGRLLLENPR 180

Qy 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNVSVYRRCPCGRMVDLNLISGI 240  
Db 181 LGSQSTNSSTYMTNTKTGLQFNTVSKLDTGEYSCEARNVSVYRRCPCGRMVDLNLISGI 240

Qy 241 IAAVVVALVISVCGLVCAQKGYFSEKTSFQKSNSSSKATTMSNDPKHTKSFII 298  
Db 241 IAAVVVALVISVCGLVCAQKGYFSEKTSFQKSNSSSKATTMSNDPKHTKSFII 298

RESULT 10  
ABU64994  
ID ABU64994 standard; protein; 298 AA.

XX AC ABU64994;  
XX AC ABU64994;  
XX DT 15-MAY-2003 (first entry)  
XX DE Human secreted protein gene 25, protein.

XX KW Secreted protein; immunodeficiency; multiple sclerosis;  
KW severe combined immunodeficiency; autoimmune disorder; cancer;  
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;  
KW inflammatory condition; septic shock; inflammatory bowel disease;  
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;  
KW gastrointestinal disorder; central nervous system disorder;  
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;  
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;  
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;  
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;  
KW endocrine disorder; liver disease; reproductive system disorder;  
KW endometriosis; infectious disease; pancreatic disorder; vaccine;  
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;

KW body height; hair colour; human.  
 XX Homo sapiens.  
 OS US2002L72994-A1.  
 XX 21-NOV-2002.  
 XX 11-MAY-2001; 2001US-00852797.  
 XX 14-MAR-1997; 97US-0040710P.  
 PR 14-MAR-1997; 97US-0040762P.  
 PR 30-MAY-1997; 97US-0048100P.  
 PR 30-MAY-1997; 97US-0048189P.  
 PR 30-MAY-1997; 97US-0048357P.  
 PR 30-MAY-1997; 97US-0050934P.  
 PR 06-JUN-1997; 97US-0048970P.  
 PR 05-SEP-1997; 97US-0057765P.  
 PR 19-DEC-1997; 97US-0068368P.  
 PR 12-MAR-1998; 98WO-US0004858.  
 PR 11-SEP-1998; 98US-00152060.  
 PR 02-FEB-2001; 2001US-0265583P.  
 XX (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (LIYU/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (KYAW/) KYAW H.  
 PA (FISC/) FISCHER C L.  
 PA (LIH/) LI H.  
 PA (SOPP/) SOPPET D R.  
 PA (GENT/) GENTZ R L.  
 PA (WEI/) WEI Y.  
 PA (MOOR/) MOORE P A.  
 PA (YOUN/) YOUNG P B.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;  
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PB, Greene JM;  
 PI Ferrie AM;  
 XX WPI: 2003-310969/30.  
 DR N-PSDB; ABX96990.  
 XX New human secreted polypeptides and polynucleotides for diagnosing,  
 PT prognosing, preventing and treating immune, hyperproliferative, liver,  
 PT kidney, reproductive disorders and for identifying modulators of  
 PT therapeutic use.  
 XX Claim 11; Page 186; 209pp; English.  
 XX The invention relates to an isolated polypeptide comprising an amino acid  
 CC sequence at least 95% identical to sequence of 28 human secreted  
 CC proteins, their fragment, polypeptide domain, epitope, secreted form,  
 CC variant, allelic variant, or species homologue, or the encoded sequence  
 CC included in ATCC 97921 and 97922. Also included are the encoding nucleic  
 CC acids, recombinant vectors, host cells, antibodies, and genes. The  
 CC proteins and nucleic acids are useful for diagnosing, preventing,  
 CC treating, prognosing or ameliorating a medical condition e.g.  
 CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell  
 CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple  
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,  
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),  
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,  
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),  
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal  
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and  
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain  
 CC injury and/or stroke, traumatic brain injury), neurodegenerative  
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related  
 CC dementia, and prion disease), cardiovascular disorders (e.g.

CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary  
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,  
 CC pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection),  
 CC blood-related disorders (thrombosis, arterial thrombosis),  
 CC hyperproliferative disorders, renal disorders (e.g. acute  
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,  
 CC hyperthyroidism, hypoparathyroidism), liver diseases and disorders,  
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,  
 CC and pancreatic disorders. Many other diseases and disorders are listed in  
 CC the specification. They also useful as a vaccine adjuvant. Further they  
 CC are useful to enhance or inhibit complement mediated cell lysis, for  
 CC stimulating wound and tissue repair, angiogenesis, and the repair of  
 CC vascular or lymphatic diseases or disorders. They are also useful to  
 CC prevent hair loss, to modulate mammalian characteristics such as body  
 CC height, weight, hair colour, and to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors or other nutritional components. The proteins are  
 CC also useful for identifying binding partners. The present sequence  
 CC represents a secreted protein of the invention  
 XX  
 SQ Sequence 298 AA;  
 Query Match 99.7%; Score 1517; DB 6; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-117; Indels 0; Gaps 0;  
 Matches 298; Conservative 0; Mismatches 0;  
 QY 1 MARRSRHRLLLRLVLLVVALGKHAYGFSAPKQDQVVTAVYQYQAILACKTPKTVASR 60  
 DB 1 MARRSRHRLLLRLVLLVVALGKHAYGFSAPKQDQVVTAVYQYQAILACKTPKTVASR 60  
 QY 61 LEWKKLGRSVFVYQQTLLQGFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQN 120  
 DB 61 LEWKKLGRSVFVYQQTLLQGFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEQQN 120  
 QY 121 LEEDTVTLVLVAPVPSCEVFSALSGTVLRCQDKGPNAPYTWFKDGIIRLENPR 180  
 DB 121 LEEDTVTLVLVAPVPSCEVFSALSGTVLRCQDKGPNAPYTWFKDGIIRLENPR 180  
 QY 181 LGSQSTNSSTYNTKTGTLQFNVTSKLDTGEYSCFARNVSVYRCPGKRMQVDDLNISGI 240  
 DB 181 LGSQSTNSSTYNTKTGTLQFNVTSKLDTGEYSCFARNVSVYRCPGKRMQVDDLNISGI 240  
 QY 241 IAAVWVVALVSVCGLVGYCARQKGYFSEKTSFQKSNSSSKATTMSNDFKHKSFI 298  
 DB 241 IAAVWVVALVSVCGLVGYCARQKGYFSEKTSFQKSNSSSKATTMSNDFKHKSFI 298  
 RESULT 11  
 ADB91670  
 ID ADB91670 standard; protein; 298 AA.  
 XX ADB91670;  
 AC ADB91670;  
 XX 04-DEC-2003 (first entry)  
 DT Human secreted protein #SEQ ID 616.  
 DE Secreted protein; gene therapy; antidiabetic; diabetes; human.  
 XX Homo sapiens.  
 OS WO2003004622-A2.  
 XX 16-JAN-2003.  
 XX 19-MAR-2002; 2002WO-US0008124.  
 XX 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Rosen CA, Ruben SM;  
 XX WPI; 2003-229407/22.  
 XX Nucleic acid encoding a human secreted protein is useful in diagnosing or  
 PT treating diabetes or conditions related to diabetes.  
 XX Claim 3; SEQ ID NO 616; 1537pp; English.  
 XX The invention relates to isolated nucleic acid molecules ADB91065-  
 CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-  
 CC ADB91834. Also disclosed is a recombinant vector comprising a  
 CC polynucleotide of the invention, and a recombinant host cell comprising  
 CC the recombinant vector. The polypeptide of the invention is useful in  
 CC identifying a binding partner by contacting the polypeptide with a  
 CC binding partner, and determining whether the binding partner increases or  
 CC decreases activity of the polypeptide. The polypeptide, polynucleotide,  
 CC antibody or its fragment, agonist or antagonist are useful for preparing  
 CC a pharmaceutical composition for diagnosing or treating diabetes or  
 CC conditions related to diabetes. The present sequence is that of the human  
 CC immunoglobulin Fc portion used to generate fusion proteins, increasing  
 CC the stability of the fused protein as compared to the secreted protein  
 CC only. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SEQ Sequence 298 AA;  
 XX  
 XX Query Match 99.7%; Score 1517; DB 7; Length 298;  
 XX Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
 XX Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXQEQAILACKTPKTVXSR 60  
 Db 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXQEQAILACKTPKTVXSR 60  
 QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
 Db 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
 QY 121 LEEDTVTLVAVAPVSCVPSSALSGTVVLRQDKEGNPAPEYTFWFGDGRILLENPR 180  
 Db 121 LEEDTVTLVAVAPVSCVPSSALSGTVVLRQDKEGNPAPEYTFWFGDGRILLENPR 180  
 QY 181 LGSQSTNSSTYNTKTGLTFQNTVSKLDTGEYSCEARNSVGVRCPGKRMQVDDLNI 240  
 Db 181 LGSQSTNSSTYNTKTGLTFQNTVSKLDTGEYSCEARNSVGVRCPGKRMQVDDLNI 240  
 QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 RESULT 12  
 ID ADC74331 standard; protein; 298 AA.  
 XX AC ADC74331;  
 XX 01-JAN-2004 (first entry)  
 XX Human secreted protein - SEQ ID 964.  
 XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
 KW antidiabetic; immunosuppressive; dermatologic; nephrotropic;  
 KW antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;  
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerrary; cytostatic;  
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
 KW parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
 KW human.

XX Homo sapiens.  
 XX WO2003038063-A2.  
 XX 08-MAY-2003.  
 XX 19-MAR-2002; 2002WO-US008277.  
 XX 21-MAR-2001; 2001US-0277340P.  
 XX 19-JUL-2001; 2001US-0306171P.  
 XX 13-NOV-2001; 2001US-0331287P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM;  
 XX WPI; 2003-430516/40.  
 XX N-PSDB; ABC73716.  
 XX New human secreted polypeptide for diagnosing, preventing or treating  
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
 PT atherosclerosis).  
 XX Claim 16; SEQ ID NO 964; 2272pp; English.  
 XX The invention relates to a novel human secreted polypeptide comprising a  
 CC defined sequence given in the specification. The polypeptide, nucleic  
 CC acid molecule, antibody, agonist or antagonist of the invention may be  
 CC useful for preparing a composition for diagnosing or treating a  
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune  
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
 CC disease, wounds and hyperproliferative disorders including  
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
 CC parasitic infections. The polypeptide may also be used during gene  
 CC therapy procedures and for identifying a binding partner by contacting  
 CC the polypeptide with a binding partner and determining whether the  
 CC binding partner increases or decreases the activity of the polypeptide.  
 CC The current sequence is that of the human secreted protein of the  
 CC invention.  
 XX SEQ Sequence 298 AA;  
 XX  
 XX Query Match 99.7%; Score 1517; DB 7; Length 298;  
 XX Best Local Similarity 100.0%; Pred. No. 1.3e-117;  
 XX Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXQEQAILACKTPKTVXSR 60  
 Db 1 MARRSRHRLLLRLVLLVVALGYHKAQFSAKDDQVVTAVXQEQAILACKTPKTVXSR 60  
 QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
 Db 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
 QY 121 LEEDTVTLVAVAPVSCVPSSALSGTVVLRQDKEGNPAPEYTFWFGDGRILLENPR 180  
 Db 121 LEEDTVTLVAVAPVSCVPSSALSGTVVLRQDKEGNPAPEYTFWFGDGRILLENPR 180  
 QY 181 LGSQSTNSSTYNTKTGLTFQNTVSKLDTGEYSCEARNSVGVRCPGKRMQVDDLNI 240  
 Db 181 LGSQSTNSSTYNTKTGLTFQNTVSKLDTGEYSCEARNSVGVRCPGKRMQVDDLNI 240  
 QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 RESULT 13  
 AAO16452

ID AAO16452 standard; protein; 298 AA.  
 AC AAO16452;  
 XX  
 DT 17-APR-2003 (first entry)  
 DE Human junctional adhesion molecule 2 (hJAM2).  
 KW Human; gene therapy; extracellular region; junctional adhesion molecules;  
 KW hJAM; immune system disorder; immune deficiency; autoimmune disorder;  
 KW inflammatory disorder; cancer; wound healing; cardiovascular disease;  
 KW full-length membrane-bound hJAM protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT Protein /label= Signal\_peptide  
 FT 29..298  
 FT Domain /note= "Mature hJAM2"  
 FT 29..236  
 FT /note= "Extracellular domain; Specifically claimed  
 FT region"  
 XX  
 PN WO2003008541-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 05-JUL-2002; 2002WO-US019800.  
 XX  
 PR 16-JUL-2001; 2001US-0305752P.  
 PR 05-FEB-2002; 2002US-0354345P.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Heuer JG, Smith RC, Su EW;  
 XX  
 DR WPI; 2003-221848/21.  
 DR N-PSDB; AAL51599.  
 XX  
 XX New extracellular human junctional adhesion molecule (hJAM) polypeptide,  
 PT useful for treating an immune system disorder such as an immune  
 PT deficiency or an inflammatory disorder, cancer, wound healing, or a  
 PT cardiovascular disease.  
 XX  
 PS Disclosure; Fig 1; 131pp; English.  
 XX  
 CC The invention comprises the DNA and protein sequences of the  
 CC extracellular region of human junctional adhesion molecules (hJAM). The  
 CC extracellular hJAM DNA and protein sequences are useful in the treatment  
 CC of: immune system disorders (e.g. immune deficiency); autoimmune  
 CC disorders; inflammatory disorders; cancer; wound healing; or a  
 CC cardiovascular disease. The present amino acid sequence represents the  
 CC full-length membrane-bound hJAM2 protein  
 XX  
 SQ Sequence 298 AA;  
 Query Match 99.5%; Score 1514; DB 6; Length 299;  
 Best Local Similarity 99.0%; Pred. No. 2.3e-117;  
 Matches 295; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MARRSRRLRLLLRLYLVALGYHKGFGSPAKDQVWTAAYQAEAILACKTPKKTVXSR 60  
 DB 1 MARRSRRLRLLLRLYLVALGYHKGFGSPAKDQVWTAAYQAEAILACKTPKKTVSR 60  
 QY 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPEQGN 120  
 DB 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPEQGN 120  
 QY 121 LEEDTVTLEVLVAPVSCVPSSALSGTVVELRCODKEGNPAPEYTFKDGIRLLENPR 180  
 DB 121 LEEDTVTLEVLVAPVSCVPSSALSGTVVELRCODKEGNPAPEYTFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCFARNVGYRRCPGKRMQVDDLNISGI 240  
 DB 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCFARNVGYRRCPGKRMQVDDLNISGI 240  
 QY 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 DB 241 IAAVVVVALVISVCGLVGYAQRKGYSKETSFOKSNSSSKATTMSSEDFKHTKSFII 298  
 RESULT 14  
 AAM23693  
 ID AAM23693 standard; protein; 303 AA.  
 XX  
 AC AAM23693;  
 XX  
 DT 12-OCT-2001 (first entry)  
 DE Human EST encoded protein SEQ ID NO: 1218.  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US002687.  
 XX  
 PR 25-JAN-2000; 2000US-00491404.  
 PR 17-JUL-2000; 2000US-00617746.  
 PR 03-AUG-2000; 2000US-00631451.  
 PR 15-SEP-2000; 2000US-00663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 DR WPI: 2001-476164/51.  
 DR N-PSDB; AAH98352.  
 XX  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use.  
 PT  
 PS Claim 20; Page 878-879; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention  
 XX  
 SQ Sequence 303 AA;  
 Query Match 98.8%; Score 1502.5; DB 4; Length 303;  
 Best Local Similarity 97.4%; Pred. No. 2.1e-116;  
 Matches 295; Conservative 1; Mismatches 2; Indels 5; Gaps 1;  
 QY 1 MARRSRRLRLLLRLYLVALGYHKGFGSPAKDQVWTAAYQAEAILACKTPKKTVXSR 60  
 DB 1 MARRSRRLRLLLRLYLVALGYHKGFGSPAKDQVWTAAYQAEAILACKTPKKTVSR 60  
 QY 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPEQGN 120  
 DB 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPEQGN 120

QY 121 LEEDTVTLVL-----VAPAVPCEVPSSALSGTVVVELRCQDKGPNAPPEYTWFKDGIRL 175  
DB 121 LEEDTVTLVLGDVHVLAPAVPCEVPSSALSGTVVVELRCQDKGPNAPPEYTWFKDGIRL 180  
QY 176 LEMPRIGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDL 235  
DB 181 LEMPRIGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDL 240  
QY 236 NISGIIAAVVVVALVSVCGLVGYAQKGYFSKETSFOKSNSSSKATTMSENDFKHTKS 295  
DB 241 NISGIIAAVVVVALVSVCGLVGYAQKGYFSKETSFOKSNSSSKATTMSENDFKHTKS 300  
QY 296 FII 298  
DB 301 FII 303  
RESULT 15  
AAY23324  
ID AAY23324 standard; protein; 312 AA.  
XX AC AAY23324;  
XX 02-SEP-1999 (first entry)  
DT A33 related antigen PRO245.  
DE A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;  
XX tumour.  
KW Homo sapiens.  
XX OS  
XX PN W09927098-A2.  
XX PD  
XX 03-JUN-1999.  
XX 20-NOV-1998; 98WO-US024855.  
XX 21-NOV-1997; 97US-0066364P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 17-SEP-1998; 98WO-US019437.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi A, Fong S, Goddard A, Gurney AL, Napier MA, Tumas D;  
PI Wood WI;  
XX  
XX WPI; 1999-404743/34.  
DR N-PSDS; AAX81770.  
XX  
XX Antigen PRO301, PRO362 and PRO245 related to A33.

Example 3; Fig 11; 122pp; English.  
The specification describes A33 related antigens PRO301, PRO362 and PRO245. The methods and compositions of the invention are useful for the treatment and diagnosis of inflammatory disease and tumours in mammals. Such inflammatory diseases include of inflammatory bowel disease, systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, scleroderma, idiopathic inflammatory myopathies, dermatomyositis, polymyositis, Sjogren's syndrome, systemic vaculitis, sarcoidosis, autoimmune hemolytic anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria, autoimmune thrombocytopenia, idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia, thyroiditis, Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis, diabetes mellitus, immune-mediated renal disease, glomerulonephritis, tubulointerstitial nephritis, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic polyneuropathy, hepatobiliary diseases, infectious hepatitis A, B, C, D, E, nonhepatotropic viruses, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy,

CC Whipple's disease, autoimmune or immune-mediated skin diseases allergic  
CC diseases of the lung such as eosinophilic pneumonias, idiopathic  
CC pulmonary fibrosis and hypersensitivity pneumonitis transplantation  
CC associated diseases disease. The present sequence represents PRO245  
XX  
SQ Sequence 312 AA;  
Query Match 96.3%; Score 1465; DB 2; Length 312;  
Best Local Similarity 99.3%; Pred. NO. 2.8e-113; Indels 0; Gaps 0;  
Matches 286; Conservative 0; Mismatches 2;  
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QY 61 LEWKKLGRSVFVYVYQOTLQGDFFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
DB 61 LEWKKLGRSVFVYVYQOTLQGDFFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
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DB 121 LEEDTVTLVLVAPAVPCEVPSSALSGTVVVELRCQDKGPNAPPEYTWFKDGIRLLENPR 180  
QY 181 LGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDLNI 240  
DB 181 LGSQSTNSGYTMTNTGTLOENTVSKLDTGEYSCEARNVGVRCPCGKRMQVDDLNI 240  
QY 241 IAAVVALVSVCGLVGYAQKGYFSKETSFOKSNSSSKATTMSEN 288  
DB 241 IAAVVALVSVCGLVGYAQKGYFSKETSFOKSNSSSKATTMSEN 288

Search completed: July 15, 2004, 23:52:46  
Job time : 81.2888 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 23:50:59 ; Search time 23.107 Seconds  
(without alignments)

Title: US-09-852-797-76

Perfect score: 1521

Sequence: 1 MARRSRHRLLLLLRYLVA.....SSKATMSENDFKHTKSFI 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of bits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 200000000

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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1: /cgm2_6/ptodata/2/iaa/5A_COMB.pcp.*
2: /cgm2_6/ptodata/2/iaa/5B_COMB.pcp.*
3: /cgm2_6/ptodata/2/iaa/6A_COMB.pcp.*
4: /cgm2_6/ptodata/2/iaa/6B_COMB.pcp.*
5: /cgm2_6/ptodata/2/iaa/PTUS_COMB.pcp.*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pcp.*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			ID	Description
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1	1517	99.7	298	4	US-09-153-060-76
2	1485	96.3	312	4	US-09-254-465A-9
3	1465	96.3	312	4	US-09-907-794A-64
4	1465	96.3	312	4	US-09-903-125A-64
5	1465	96.3	312	4	US-09-902-775A-64
6	481	31.6	310	4	US-09-907-794A-423
7	481	31.6	310	4	US-09-905-125A-423
8	481	31.6	310	4	US-09-902-775A-423
9	429	28.2	299	3	US-09-188-930-189
10	429	28.2	299	3	US-09-188-930-331
11	429	28.2	299	4	US-09-463-270-2
12	429	28.2	299	4	US-09-254-465A-1
13	429	28.2	299	4	US-09-312-283C-189
14	429	28.2	299	4	US-09-312-283C-331
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17	429	28.2	299	4	US-09-902-775A-119
18	421	27.7	300	4	US-09-254-465A-10
19	399	26.2	260	4	US-09-254-465A-23
20	399	26.2	263	4	US-09-254-465A-25
21	271.5	17.9	205	4	US-09-462-270-4
22	231	15.2	270	4	US-09-254-465A-24
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24	231	15.2	319	1	US-08-597-495B-22
25	231	15.2	319	3	US-09-068-051A-22
26	231	15.2	319	4	US-09-336-535-67
27	231	15.2	319	4	US-09-254-465A-6

## ALIGNMENTS

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Query Match 99.7%; Score 1517; DB 4; Length 298;  
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Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVXQBAAILACKTPKKTYSR 60  
Db 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVXQBAAILACKTPKKTYSR 60  
QY 61 LEWKLGSRVSFVYQOQLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
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QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180  
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QY 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNTSGI 240  
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Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFKQSNSSSKATTMSSEDFXHTKSFI 298

RESULT 2

US-09-254-465A-9  
; Sequence 9, Application US/09254465A  
; Patent No. 6410708  
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS  
; FILE REFERENCE: P12161(US)  
; CURRENT APPLICATION NUMBER: US/09/254.465A

; PRIOR APPLICATION NUMBER: 1999-03-05  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 30  
; SEQ ID NO 9  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-254-465A-9  
Query Match 96.3%; Score 1465; DB 4; Length 312;  
Best Local Similarity 99.3%; Pred. No. 1.6e-136;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

*Good date*

QY 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVXQBAAILACKTPKKTYSR 60  
Db 1 MARRSRHRLLLRLVVALGYHKAQFSAKQDQVTVAVXQBAAILACKTPKKTYSR 60  
QY 61 LEWKLGSRVSFVYQOQLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
Db 61 LEWKLGSRVSFVYQOQLQGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180  
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLRQDKEGNPAPEYTWFKDGIRLLENPR 180  
QY 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNTSGI 240  
Db 181 LGSQSTNSSYTNTKTGTLOFNTVSKLDTGEYSCEARNVGYRCPGKRMQVDDLNTSGI 240

QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFKQSNSSSKATTMSSEDFXHTKSFI 288  
Db 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFKQSNSSSKATTMSSEDFXHTKSFI 288

RESULT 3

US-09-907-794A-64  
; Sequence 64, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillen, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907.794A

; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRRLRLLLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVXSR 60
DB 1 MARRSRRLRLLLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPEQGN 120
DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPEQGN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGLTQFNTVSKLDTGEYSCEARNVGYRRCPCGRMQVDDLNISGI 240
DB 181 LGSQSTNSSYTMNTKTGLTQFNTVSKLDTGEYSCEARNVGYRRCPCGRMQVDDLNISGI 240
QY 241 IAAVVVALVISVCGLGVCYQAKRGYFSKETSFQKSNSSSKATTMSN 288
DB 241 IAAVVVALVISVCGLGVCYQAKRGYFSKETSFQKSNSSSKATTMSN 288

RESULT 4
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-136;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRRLRLLLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVXSR 60
DB 1 MARRSRRLRLLLRLVVALGYHKAQFSAKQDQVVTAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPEQGN 120
DB 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPEQGN 120
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVLELRCQDKEGNAPEYTWFKDGIRLLENPR 180
QY 181 LGSQSTNSSYTMNTKTGLTQFNTVSKLDTGEYSCEARNVGYRRCPCGRMQVDDLNISGI 240
DB 181 LGSQSTNSSYTMNTKTGLTQFNTVSKLDTGEYSCEARNVGYRRCPCGRMQVDDLNISGI 240
QY 241 IAAVVVALVISVCGLGVCYQAKRGYFSKETSFQKSNSSSKATTMSN 288
DB 241 IAAVVVALVISVCGLGVCYQAKRGYFSKETSFQKSNSSSKATTMSN 288

RESULT 5
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 668451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

/ APPLICANT: Filvaroff, Ellen  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerbittsen, Mary E.  
 / APPLICANT: Goddard, A.  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth, J.  
 / APPLICANT: Kljavin, Ivar J.  
 / APPLICANT: Mather, Jennie P.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William, I.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / TITLE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: 10466-14  
 / CURRENT APPLICATION NUMBER: US/09/902,775A  
 / CURRENT FILING DATE: 2001-07-10  
 / PRIOR APPLICATION NUMBER: PCT/US00/04414  
 / PRIOR FILING DATE: 2000-02-22  
 / PRIOR APPLICATION NUMBER: US 60/143,048  
 / PRIOR FILING DATE: 1999-07-07  
 / PRIOR APPLICATION NUMBER: US 60/145,698  
 / PRIOR FILING DATE: 1999-07-26  
 / PRIOR APPLICATION NUMBER: US 60/146,222  
 / PRIOR FILING DATE: 1999-07-28  
 / PRIOR APPLICATION NUMBER: PCT/US99/20594  
 / PRIOR FILING DATE: 1999-08-08  
 / PRIOR APPLICATION NUMBER: PCT/US99/20944  
 / PRIOR FILING DATE: 1999-09-13  
 / PRIOR APPLICATION NUMBER: PCT/US99/21090  
 / PRIOR FILING DATE: 1999-09-15  
 / PRIOR APPLICATION NUMBER: PCT/US99/21547  
 / PRIOR FILING DATE: 1999-09-15  
 / PRIOR APPLICATION NUMBER: PCT/US99/21547  
 / PRIOR FILING DATE: 1999-09-15  
 / PRIOR APPLICATION NUMBER: PCT/US99/23089  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: PCT/US99/28214  
 / PRIOR FILING DATE: 1999-11-30  
 / PRIOR APPLICATION NUMBER: PCT/US99/28564  
 / PRIOR FILING DATE: 1999-12-02  
 / PRIOR APPLICATION NUMBER: PCT/US99/28565  
 / PRIOR FILING DATE: 1999-12-02  
 / PRIOR APPLICATION NUMBER: PCT/US99/30095  
 / PRIOR FILING DATE: 1999-12-16  
 / PRIOR APPLICATION NUMBER: PCT/US99/30911  
 / PRIOR FILING DATE: 1999-12-20  
 / PRIOR APPLICATION NUMBER: PCT/US99/30999  
 / PRIOR FILING DATE: 1999-12-20  
 / PRIOR APPLICATION NUMBER: PCT/US00/00219  
 / PRIOR FILING DATE: 2000-01-05  
 / NUMBER OF SEQ ID NOS: 423  
 / SEQ ID NO 64  
 / LENGTH: 312  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-902-775A-64

Query Match 96.3%; Score 1465; DB 4; Length 312;  
 Best Local Similarity 99.3%; Pred. No. 1.6e-136;  
 Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MARRSRHLLLLRLVVALGYHKYGFSAKDDQVVTVXVYCEAILACKTPKTKYXSR 60  
 DB 1 MARRSRHLLLLRLVVALGYHKYGFSAKDDQVVTVXVYCEAILACKTPKTKYXSR 60

QY 61 LEWKLLGRSVSVFYQOTLQGDFFKRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSQGN 120  
 DB 61 LEWKLLGRSVSVFYQOTLQGDFFKRAEMIDFNIRIKNVTNRSDAGKYRCEVSAPSQGN 120  
 QY 121 LEEDTTLVLVAPVPSCEVPSSALSGTVLRLCQDKEGNPAPEYTWFKDGIRLLENPR 180  
 DB 121 LEEDTTLVLVAPVPSCEVPSSALSGTVLRLCQDKEGNPAPEYTWFKDGIRLLENPR 180  
 QY 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEVSCSEARNVSVYRRCGKRMQVDDNLNIGI 240  
 DB 181 LGSQSTNSSYTMNTKTGLQFNTVSKLDTGEVSCSEARNVSVYRRCGKRMQVDDNLNIGI 240  
 QY 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKNSSSSKATTMSEN 288  
 DB 241 IAAVVVALVISVCGLVGYAQRKGYFSKETSFOKNSSSSKATTMSEN 288  
 RESULT 6  
 US-09-907-794A-423  
 / Sequence 423, Application US/09907794A  
 / Patent No. 6635468  
 / GENERAL INFORMATION:  
 / APPLICANT: Genentech, Inc.  
 / APPLICANT: Ashkenazi, Avi  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Filvaroff, Ellen  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerbittsen, Mary E.  
 / APPLICANT: Goddard, A.  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth, J.  
 / APPLICANT: Kljavin, Ivar J.  
 / APPLICANT: Mather, Jennie P.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William, I.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / TITLE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: 10466-14  
 / CURRENT APPLICATION NUMBER: US/09/907,794A  
 / CURRENT FILING DATE: 2001-07-17  
 / PRIOR APPLICATION NUMBER: PCT/US00/04414  
 / PRIOR FILING DATE: 2000-02-22  
 / PRIOR APPLICATION NUMBER: US 60/143,048  
 / PRIOR FILING DATE: 1999-07-07  
 / PRIOR APPLICATION NUMBER: US 60/145,698  
 / PRIOR FILING DATE: 1999-07-26  
 / PRIOR APPLICATION NUMBER: US 60/146,222  
 / PRIOR FILING DATE: 1999-07-28  
 / PRIOR APPLICATION NUMBER: PCT/US99/20594  
 / PRIOR FILING DATE: 1999-09-08  
 / PRIOR APPLICATION NUMBER: PCT/US99/20944  
 / PRIOR FILING DATE: 1999-09-13  
 / PRIOR APPLICATION NUMBER: PCT/US99/21090  
 / PRIOR FILING DATE: 1999-09-15  
 / PRIOR APPLICATION NUMBER: PCT/US99/21547  
 / PRIOR FILING DATE: 1999-09-15  
 / PRIOR APPLICATION NUMBER: PCT/US99/23089  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: PCT/US99/28214  
 / PRIOR FILING DATE: 1999-11-29  
 / PRIOR APPLICATION NUMBER: PCT/US99/28313

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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match      31.6%; Score 481; DB 4; Length 310;
Best Local Similarity 35.8%; Pred. No. 2.5e-39;
Matches 114; Conservative 60; Mismatches 116; Indels 28; Gaps 10;

QY 1 MARRSRRL-----LILLRLYLVALGYHKAQFSAKPKDQOVTVAVYQAILAC 50
DB 1 MALRRPRLRLCARLPDPFLLLFGRCLIG-----AVNLKSNRTPVQ--EFESVELSC 53

QY 51 -KTPKKTVXSRLWKKL-GRSVSFVYVYQOTLQDGFKNRAEMI-DFNIRIKNVTSDAGKY 107
DB 54 IITDSQTSDFRIEWKKIQDQTTVFFDNKIQDGLAGRAEILGKTSLKINVTNRDSALY 113

QY 108 RCEVAPSSEQQNLEEDTIVLEVAVAPVSPCEVPSSALSGTVVLELRCQKGNPAPEYT 167
DB 114 RCEVVARNDR-KEIDEIVIELTVQKPTVPCVEPKAVPVGKMATLHCQESGHPHYS 172

QY 168 WFKDGIILLENPLRGSQSTNSSTYNTKTGTLOFTVSKLDTGEYSCEARNVGYRCPG 227
DB 173 WYRNDVPLPTDSRANPRFNSFHLNSETGTTLVFTAVHKDSDGQYCIASNDAGSARCEE 232

QY 281 KATTMSNDKHTKSFII 298
DB 293 YIRDEGDFHKSFSVII 310

RESULT 7
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

[illegible]

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Db      5 AOVERKLLCLFILAILLCSALGSLGSGVTVHSSEPEVRIPENNPVKLSAYS-----GFSSP-- 58
QY      56 TVXSRLEWK-KLGRSVFVYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCVVSAP 114
Db      59 ----RVWKPDQDGTTLVLCYNKKITASYEDRVTFPTGITFSVTRDGTGTYTCMVS-- 112
QY      115 SEQQNLEEDTVTLVLVAVPSCVPSGALSGTVVLRCDQKGNPAPEYTFWKDGIR 174
Db      113 EEGNSYGEVKVLIVLPSPKPTVNPSSATIGNRAVLTCSEQDGSPPSEYTFWKDGIV 172
QY      175 LLENPRLGSTNSSTYMTNTKTGLQFNVTYSKLDTGYSCEARNVGYRRCPCGK-RMQVD 233
Db      173 MPTNPKSTRAFNSSYVLPNTTIGELVDFPLSADTGYSCEARNGYGTPTMSNAVRMEAV 232
QY      234 DLNLSGIIAAVVVVALVISVCGLVGYCAQRKGYSKTSFKQNSSSKA-----TTMSEN 288
Db      233 ERNVGVIAAVALVTXILLGILVFGIWFAYSRGHFDRT---KGTSSKKVIYQPSARSEX 289
QY      289 DFKHTKSFI 298
Db      290 EFKQTSSFLV 299

RESULT 10
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match      28.2%; Score 429; DB 3; Length 299;
Best Local Similarity 34.2%; Pred. No. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;

QY      2 ARSRHRLLLLRVLLVVALGYHKAYGFS-----PKDQVVTAVXYQAILLACKTPKK 55
Db      5 AOVERKLLCLFILAILLCSALGSLGSGVTVHSSEPEVRIPENNPVKLSAYS-----GFSSP-- 58
QY      56 TVXSRLEWK-KLGRSVFVYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCVVSAP 114
Db      59 ----RVWKPDQDGTTLVLCYNKKITASYEDRVTFPTGITFSVTRDGTGTYTCMVS-- 112
QY      115 SEQQNLEEDTVTLVLVAVPSCVPSGALSGTVVLRCDQKGNPAPEYTFWKDGIR 174
Db      113 EEGNSYGEVKVLIVLPSPKPTVNPSSATIGNRAVLTCSEQDGSPPSEYTFWKDGIV 172
QY      175 LLENPRLGSTNSSTYMTNTKTGLQFNVTYSKLDTGYSCEARNVGYRRCPCGK-RMQVD 233
Db      173 MPTNPKSTRAFNSSYVLPNTTIGELVDFPLSADTGYSCEARNGYGTPTMSNAVRMEAV 232
QY      234 DLNLSGIIAAVVVVALVISVCGLVGYCAQRKGYSKTSFKQNSSSKA-----TTMSEN 288
Db      233 ERNVGVIAAVALVTXILLGILVFGIWFAYSRGHFDRT---KGTSSKKVIYQPSARSEX 289
QY      289 DFKHTKSFI 298
Db      290 EFKQTSSFLV 299

RESULT 11
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human FII Antigen: A Cell Surface
; FILE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match      28.2%; Score 429; DB 4; Length 299;
Best Local Similarity 34.2%; Pred. No. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;

QY      2 ARSRHRLLLLRVLLVVALGYHKAYGFS-----PKDQVVTAVXYQAILLACKTPKK 55
Db      5 AOVERKLLCLFILAILLCSALGSLGSGVTVHSSEPEVRIPENNPVKLSAYS-----GFSSP-- 58
QY      56 TVXSRLEWK-KLGRSVFVYQOTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCVVSAP 114
Db      59 ----RVWKPDQDGTTLVLCYNKKITASYEDRVTFPTGITFSVTRDGTGTYTCMVS-- 112
QY      115 SEQQNLEEDTVTLVLVAVPSCVPSGALSGTVVLRCDQKGNPAPEYTFWKDGIR 174
Db      113 EEGNSYGEVKVLIVLPSPKPTVNPSSATIGNRAVLTCSEQDGSPPSEYTFWKDGIV 172
QY      175 LLENPRLGSTNSSTYMTNTKTGLQFNVTYSKLDTGYSCEARNVGYRRCPCGK-RMQVD 233
Db      173 MPTNPKSTRAFNSSYVLPNTTIGELVDFPLSADTGYSCEARNGYGTPTMSNAVRMEAV 232
QY      234 DLNLSGIIAAVVVVALVISVCGLVGYCAQRKGYSKTSFKQNSSSKA-----TTMSEN 288
Db      233 ERNVGVIAAVALVTXILLGILVFGIWFAYSRGHFDRT---KGTSSKKVIYQPSARSEX 289
QY      289 DFKHTKSFI 298
Db      290 EFKQTSSFLV 299

RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; FILE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
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; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match      28.2%; Score 429; DB 4; Length 299;
Best Local Similarity 34.2%; Pred. No. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;

QY 2 ARSRHRLLLRLVVALGVHKGAYGFS-----PKDQOVVTAVYQEAAILACKTPKK 55
DB 5 AQVERKLLCLFILAILLCSLALGVTVHSSPEFVRIPENNPKLSCAYS----GFSSP-- 58
QY 56 TVXSRLWK-KLGRSVSVFYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
DB 59 ----RVEMKFDQDITRLVCYNNKITASYEDRVTFPLTGITFKSVTRDTGTYTCMVS-- 112
QY 115 SEQGNLEEDTTLVLVAVAPVSPSSALSGTVVLRQDKEGNPAPEYTWFKDGIR 174
DB 113 EGGNSYGEVKVLIIVLPSPKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIV 172
QY 175 LLENPLGQSSTNSYTNKTGTLOFNTVSKLDTGEYSCARNVSVGYRRCPGK-RMQVD 233
DB 173 MPTNPKSTRAFNSNYSVLNPTTGELVDFPLSDTGEYSCARNYGTPTMSTNAVRMEAV 232
QY 234 DLNISGIIAAVVVALVISVCGLVGYCAQRKGYSKETSFOKSNSSSKA-----TTMSEN 288
DB 233 ERNVGVIVAALVTLILLGILVFGIWFAYSRGHFDR---KKGTSKKVIYQSPARSEG 289
QY 289 DFKHTKSFII 298
DB 290 EFKQTSSFLV 299

RESULT 14
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-331

Query Match      28.2%; Score 429; DB 4; Length 299;
Best Local Similarity 34.2%; Pred. No. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;

QY 2 ARSRHRLLLRLVVALGVHKGAYGFS-----PKDQOVVTAVYQEAAILACKTPKK 55
DB 5 AQVERKLLCLFILAILLCSLALGVTVHSSPEFVRIPENNPKLSCAYS----GFSSP-- 58
QY 56 TVXSRLWK-KLGRSVSVFYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
DB 59 ----RVEMKFDQDITRLVCYNNKITASYEDRVTFPLTGITFKSVTRDTGTYTCMVS-- 112
QY 115 SEQGNLEEDTTLVLVAVAPVSPSSALSGTVVLRQDKEGNPAPEYTWFKDGIR 174
DB 113 EGGNSYGEVKVLIIVLPSPKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIV 172
QY 175 LLENPLGQSSTNSYTNKTGTLOFNTVSKLDTGEYSCARNVSVGYRRCPGK-RMQVD 233
DB 173 MPTNPKSTRAFNSNYSVLNPTTGELVDFPLSDTGEYSCARNYGTPTMSTNAVRMEAV 232
QY 234 DLNISGIIAAVVVALVISVCGLVGYCAQRKGYSKETSFOKSNSSSKA-----TTMSEN 288
DB 233 ERNVGVIVAALVTLILLGILVFGIWFAYSRGHFDR---KKGTSKKVIYQSPARSEG 289
QY 289 DFKHTKSFII 298
DB 290 EFKQTSSFLV 299

RESULT 13
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-189

Query Match      28.2%; Score 429; DB 4; Length 299;
Best Local Similarity 34.2%; Pred. No. 3.2e-34;
Matches 106; Conservative 50; Mismatches 126; Indels 28; Gaps 8;

QY 2 ARSRHRLLLRLVVALGVHKGAYGFS-----PKDQOVVTAVYQEAAILACKTPKK 55
DB 5 AQVERKLLCLFILAILLCSLALGVTVHSSPEFVRIPENNPKLSCAYS----GFSSP-- 58
QY 56 TVXSRLWK-KLGRSVSVFYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP 114
DB 59 ----RVEMKFDQDITRLVCYNNKITASYEDRVTFPLTGITFKSVTRDTGTYTCMVS-- 112
QY 115 SEQGNLEEDTTLVLVAVAPVSPSSALSGTVVLRQDKEGNPAPEYTWFKDGIR 174
DB 113 EGGNSYGEVKVLIIVLPSPKPTVNIPISSATIGNRAVLTCSEQDGPSPSEYTWFKDGIV 172
QY 175 LLENPLGQSSTNSYTNKTGTLOFNTVSKLDTGEYSCARNVSVGYRRCPGK-RMQVD 233
DB 173 MPTNPKSTRAFNSNYSVLNPTTGELVDFPLSDTGEYSCARNYGTPTMSTNAVRMEAV 232
QY 234 DLNISGIIAAVVVALVISVCGLVGYCAQRKGYSKETSFOKSNSSSKA-----TTMSEN 288
DB 233 ERNVGVIVAALVTLILLGILVFGIWFAYSRGHFDR---KKGTSKKVIYQSPARSEG 289
QY 289 DFKHTKSFII 298
DB 290 EFKQTSSFLV 299
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:54:34 ; Search time 64.5401 Seconds  
(without alignments)  
1443.181 Million cell updates/sec

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Perfect score: 1521  
Sequence: 1 MAARRRHLRLLLRLVLA.....SSKATTMSNDPHTKSFII 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

- Database :
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  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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  - 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1518	99.8	298	9	US-09-745-763-38
2	1518	99.8	298	9	US-09-799-777-30
3	1518	99.8	298	14	US-10-139-849-2
4	1518	99.8	298	14	US-10-192-791-2
5	1518	99.8	298	16	US-10-601-953-889
6	1517	99.7	298	9	US-09-853-161-76
7	1517	99.7	298	9	US-09-852-659A-76
8	1517	99.7	298	9	US-09-852-797-76
9	1517	99.7	298	12	US-10-058-993-76
10	1465	96.3	312	9	US-09-909-320-64
11	1465	96.3	312	9	US-09-909-0888-64
12	1465	96.3	312	9	US-09-905-291A-64
13	1465	96.3	312	9	US-09-953-499-9
14	1465	96.3	312	9	US-09-902-853-64
15	1465	96.3	312	9	US-09-907-824-64

16	1465	96.3	312	9	US-09-907-841-64
17	1465	96.3	312	10	US-09-904-011-64
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19	1465	96.3	312	10	US-09-906-838-64
20	1465	96.3	312	10	US-09-907-613-64
21	1465	96.3	312	10	US-09-907-942-64
22	1465	96.3	312	10	US-09-904-859-64
23	1465	96.3	312	10	US-09-909-204-64
24	1465	96.3	312	10	US-09-904-820-64
25	1465	96.3	312	10	US-09-904-786-64
26	1465	96.3	312	10	US-09-906-646-64
27	1465	96.3	312	10	US-09-906-700-64
28	1465	96.3	312	10	US-09-903-786-64
29	1465	96.3	312	10	US-09-902-903-64
30	1465	96.3	312	10	US-09-903-749A-64
31	1465	96.3	312	10	US-09-904-119-64
32	1465	96.3	312	10	US-09-904-356-64
33	1465	96.3	312	10	US-09-902-736-64
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36	1465	96.3	312	10	US-09-904-462-64
37	1465	96.3	312	10	US-09-907-925-64
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40	1465	96.3	312	10	US-09-905-056-64
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44	1465	96.3	312	10	US-09-905-088-64
45	1465	96.3	312	10	US-09-907-575-64

ALIGNMENTS

RESULT 1  
US-09-745-763-38  
; Sequence 38, Application US/09745763  
; Patent No. US20020065394A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; McCoy, John M.  
; Lavallie, Edward R.  
; Collins-Racie, Lisa A.  
; Evans, Cheryl  
; Merberg, David  
; Treacy, Maurice  
; Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 219  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/745,763  
; APPLICATION NUMBER: US/09/745,763  
; FILING DATE: 18-Jun-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprunger, Suzanne A.  
; REGISTRATION NUMBER: 41,323  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8284  
; TELEFAX: (617) 876-5851

Hand date



TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-139-849-2

Query Match 99.8%; Score 1518; DB 14; Length 298;  
Best Local Similarity 99.3%; Pred. No. 1.4e-135;  
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 MARRSRHLLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60  
QY 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
DB 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPR 180  
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPR 180  
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DB 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCAARNVGYRRCPCGRMQVDDNLNISI 240  
QY 241 IAAVVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298  
DB 241 IAAVVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298

RESULT 4  
US-10-192-791-2  
; Sequence 2, Application US/10192791  
; Publication No. US20030130166A1  
; GENERAL INFORMATION:  
; APPLICANT: Texas Biotechnology Corporation  
; TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (JA  
; FILE REFERENCE: TX4542P0430  
; CURRENT APPLICATION NUMBER: US/10/192,791  
; CURRENT FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-192-791-2

Query Match 99.8%; Score 1518; DB 14; Length 298;  
Best Local Similarity 99.3%; Pred. No. 1.4e-135;  
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 MARRSRHLLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60  
QY 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
DB 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPR 180  
DB 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIIRLLENPR 180  
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DB 181 LGSQSTNSSYTMNTKTGTQLQNTVSKLDTGEYSCAARNVGYRRCPCGRMQVDDNLNISI 240

QY 241 IAAVVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298  
DB 241 IAAVVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298  
RESULT 5  
US-10-601-953-889  
; Sequence 889, Application US/10601953  
; Publication No. US20040077540A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial  
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of  
; TITLE OF INVENTION: Therapeutic Compounds  
; FILE REFERENCE: 02-0305  
; CURRENT APPLICATION NUMBER: US/10/601,953  
; CURRENT FILING DATE: 2003-06-24  
; PRIOR APPLICATION NUMBER: 60/392,512  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 889  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-601-953-889  
Query Match 99.8%; Score 1518; DB 16; Length 298;  
Best Local Similarity 99.3%; Pred. No. 1.4e-135;  
Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 MARRSRHLLLLRLYLVALGKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60  
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DB 61 LEWKKLGRSVFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
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DB 241 IAAVVVVVALVISVCGLVGVCYQAKRGYFSKETSFOKSNSSSKATTMSNDPKHTKSFII 298

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RESULT 6  
US-09-853-161-76  
; Sequence 76, Application US/09853161  
; Patent No. US20020076756A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 28 Human Secreted Proteins  
; FILE REFERENCE: P2003P3  
; CURRENT APPLICATION NUMBER: US/09/853,161  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/265,583  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/152,060  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: PCT/US98/04858  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/040,762  
; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710  
; PRIOR FILING DATE: 1997-03-14  
; PRIOR APPLICATION NUMBER: 60/050,934  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,100  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,357  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,189  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/057,765  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,368  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (42)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (58)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-853-161-76

Query Match 99.7%; Score 1517; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-135;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 181 LGSQSTNSSYTNTKTGTLPQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240  
Db 181 LGSQSTNSSYTNTKTGTLPQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240  
QY 241 IAAVWVALVSVCGLVGYCAQRKGYFSKTSFQKSNSSKATMTSENDFKHTKSFII 298  
Db 241 IAAVWVALVSVCGLVGYCAQRKGYFSKTSFQKSNSSKATMTSENDFKHTKSFII 298

RESULT 7  
US-09-852-659A-76  
; Sequence 76, Application US/09852659A  
; Patent No. US20020077287A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 28 Human Secreted Proteins  
; FILE REFERENCE: PZ003P4  
; CURRENT APPLICATION NUMBER: US/09/852,659A  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/265,583  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/152,050  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: PCT/US98/04858  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14  
; PRIOR APPLICATION NUMBER: 60/040,710  
; PRIOR FILING DATE: 1997-03-14  
; PRIOR APPLICATION NUMBER: 60/050,934  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,100  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,357  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,189  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/057,765  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,368  
; PRIOR FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (42)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (58)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-852-659A-76

Query Match 99.7%; Score 1517; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-135;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARRSRHRLLLRLVVALGYHKAIGFSAKQVQVAVXYQAEILACKTPKKTYSR 60  
Db 1 MARRSRHRLLLRLVVALGYHKAIGFSAKQVQVAVXYQAEILACKTPKKTYSR 60  
QY 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
Db 61 LEWKLGSRVSFVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN 120  
QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPETWFKDGIRLLENPR 180  
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQKEGNPAPETWFKDGIRLLENPR 180  
QY 181 LGSQSTNSSYTNTKTGTLPQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240  
Db 181 LGSQSTNSSYTNTKTGTLPQNTVSKLDTGEYSCEARNVGYRRCPCGKRMQVDDLNI 240  
QY 241 IAAVWVALVSVCGLVGYCAQRKGYFSKTSFQKSNSSKATMTSENDFKHTKSFII 298  
Db 241 IAAVWVALVSVCGLVGYCAQRKGYFSKTSFQKSNSSKATMTSENDFKHTKSFII 298

RESULT 8  
US-09-852-797-76  
; Sequence 76, Application US/09852797  
; Patent No. US20020172994A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 28 Human Secreted Proteins  
; FILE REFERENCE: PZ003P2  
; CURRENT APPLICATION NUMBER: US/09/852,797  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/265,583  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/152,060  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any amino acid
; US-10-058-993-76

Query Match
Best Local Similarity 99.7%; Score 1517; DB 12; Length 298;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRRLRLLLRLVVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VXS R 60
Db 1 MARRSRRLRLLLRLVVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VXS R 60
QY 61 LEWKKLGRSVSFVYVYQQT LQGD FKNRAE MIDFNIR IKNVTRSDAGKYRCEVSAPSEOGQN 120
Db 61 LEWKKLGRSVSFVYVYQQT LQGD FKNRAE MIDFNIR IKNVTRSDAGKYRCEVSAPSEOGQN 120
QY 121 LEEDTVTLVLVAPVSPCEVPSSALSGT VVELRCQDKEG NPAPEYTWFKDGI RLL ENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGT VVELRCQDKEG NPAPEYTWFKDGI RLL ENPR 180
QY 181 LGSQSTNSSYTMNTKTGT LQNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGT LQNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNISGI 240
QY 241 IAAVWVVALVISVCGLGVCY AQRKG YFSKETS FQKSNSSSKATTMS ENDFKHTKSFII 298
Db 241 IAAVWVVALVISVCGLGVCY AQRKG YFSKETS FQKSNSSSKATTMS ENDFKHTKSFII 298

RESULT 10
US-09-909-320-64
; Sequence 64, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 76
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-852-797-76

Query Match
Best Local Similarity 99.7%; Score 1517; DB 9; Length 298;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSRRLRLLLRLVVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VXS R 60
Db 1 MARRSRRLRLLLRLVVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VXS R 60
QY 61 LEWKKLGRSVSFVYVYQQT LQGD FKNRAE MIDFNIR IKNVTRSDAGKYRCEVSAPSEOGQN 120
Db 61 LEWKKLGRSVSFVYVYQQT LQGD FKNRAE MIDFNIR IKNVTRSDAGKYRCEVSAPSEOGQN 120
QY 121 LEEDTVTLVLVAPVSPCEVPSSALSGT VVELRCQDKEG NPAPEYTWFKDGI RLL ENPR 180
Db 121 LEEDTVTLVLVAPVSPCEVPSSALSGT VVELRCQDKEG NPAPEYTWFKDGI RLL ENPR 180
QY 181 LGSQSTNSSYTMNTKTGT LQNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGT LQNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNISGI 240
QY 241 IAAVWVVALVISVCGLGVCY AQRKG YFSKETS FQKSNSSSKATTMS ENDFKHTKSFII 298
Db 241 IAAVWVVALVISVCGLGVCY AQRKG YFSKETS FQKSNSSSKATTMS ENDFKHTKSFII 298

RESULT 9
US-10-058-993-76
; Sequence 76, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ00395
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11





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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-64

Query Match          96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEOGQN 120
Db 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNSVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNSVGYRCPGKRMQVDDLNISGI 240

QY 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKNSSSSKATTMSN 288
Db 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKNSSSSKATTMSN 288
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RESULT 12

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US-09-905-291A-64
; Sequence 64, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

```
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905.291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-64

Query Match          96.3%; Score 1465; DB 9; Length 312;
Best Local Similarity 99.3%; Pred. No. 1.6e-130;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSR 60
Db 1 MARRSRHRLLLRLYLVALGYHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVSSR 60

QY 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEOGQN 120
Db 61 LEWKLGSRVSFVYQOQTLOGDFKNRAEMIDFNIRKNVTRSDAGKYRCEVSAPSEOGQN 120

QY 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180
Db 121 LEEDTVTLVLVAPVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR 180

QY 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNSVGYRCPGKRMQVDDLNISGI 240
Db 181 LGSQSTNSSYTMNTKTGTLQFNVTSKLDTGEYSCEARNSVGYRCPGKRMQVDDLNISGI 240

QY 241 IAAVVVVALVISVCGLGVCYAQRKGYSFKTSFKNSSSSKATTMSN 288
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Db 241 IAAVVVALVSVGLGVCYQAKRGYFSGKTSFQKSNSSSKATTMSEN 288  
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## RESULT 13

US-09-953-499-9  
; Sequence 9, Application US/09953499  
; Publication No. US20020182206A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT  
; OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS  
; FILE REFERENCE: P1216R1(US)  
; CURRENT APPLICATION NUMBER: US/09/953,499  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: US/09/254,465  
; PRIOR FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: PCT/US98/24855  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: US 60/066,364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: US 60/078,936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/US98/19437  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 30  
; SEQ ID NO 9  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-953-499-9

Query Match 96.3%; Score 1465; DB 9; Length 312;  
Best Local Similarity 99.3%; Pred. No. 1.6e-130;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VYXR 60  
|||  
Db 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VYSSR 60  
|||  
QY 61 LEWKLGSRVSFVYVYQQTLOQDFKNRAEMIDFNIRIKNVTRSDAGKYRCVSPSQGQN 120  
|||  
Db 61 LEWKLGSRVSFVYVYQQTLOQDFKNRAEMIDFNIRIKNVTRSDAGKYRCVSPSQGQN 120  
|||  
QY 121 LEEDTVLEVLVAPVSPCEVPVSALSGTVVLELRCQKGNPAPEYTWFKDGRLLLENPR 180  
|||  
Db 121 LEEDTVLEVLVAPVSPCEVPVSALSGTVVLELRCQKGNPAPEYTWFKDGRLLLENPR 180  
|||  
QY 181 LGSOSTNSSYTMNTKTGLTFNTVSKLDTGEYSCEARNVGYRRCRKNQVDDLNISGI 240  
|||  
Db 181 LGSOSTNSSYTMNTKTGLTFNTVSKLDTGEYSCEARNVGYRRCRKNQVDDLNISGI 240  
|||  
QY 241 IAAVVVALVSVGLGVCYQAKRGYFSGKTSFQKSNSSSKATTMSEN 288  
|||||  
Db 241 IAAVVVALVSVGLGVCYQAKRGYFSGKTSFQKSNSSSKATTMSEN 288  
|||||

## RESULT 14

US-09-902-853-64  
; Sequence 64, Application US/09902853  
; Publication No. US20020192659A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
Query Match 96.3%; Score 1465; DB 9; Length 312;  
Best Local Similarity 99.3%; Pred. No. 1.6e-130;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MARRSRHRLLLRLYLVALGYHKA YGFSAPKDDQVVTA VYQEA ILLACKTPKKT VYXR 60  
|||||

Db 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60  
QY 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120  
Db 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120  
QY 121 LEEDTVTLVLVAPAVPSCVPSALSGLTGTQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 180  
Db 121 LEEDTVTLVLVAPAVPSCVPSALSGLTGTQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 180  
QY 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 240  
Db 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 240  
QY 241 IAAVVVVVALVISVCGLVGCYQAQRKGYFSKETSFKQSNSSSKATTMSEN 288  
Db 241 IAAVVVVVALVISVCGLVGCYQAQRKGYFSKETSFKQSNSSSKATTMSEN 288

RESULT 15

US-09-907-824-64  
; Sequence 64, Application US/09907824  
; Publication No. US20020197671A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paori, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,824  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/665,350  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 64  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-907-824-64  
  
Query Match 96.3%; Score 1465; DB 9; Length 312;  
Best Local Similarity 99.3%; Pred. No. 1.6e-130;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60  
Db 1 MARRSRHRLLLRLYLVALGYHKAQFSAKQDQVTVAVEYQEAAILACKTPKKTVSSR 60  
QY 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120  
Db 61 LEWKKLGRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGN 120  
QY 121 LEEDTVTLVLVAPAVPSCVPSALSGLTGTQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 180  
Db 121 LEEDTVTLVLVAPAVPSCVPSALSGLTGTQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 180  
QY 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 240  
Db 181 LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCARNVGYRRCCKRMQVDDDLNISI 240  
QY 241 IAAVVVVVALVISVCGLVGCYQAQRKGYFSKETSFKQSNSSSKATTMSEN 288  
Db 241 IAAVVVVVALVISVCGLVGCYQAQRKGYFSKETSFKQSNSSSKATTMSEN 288

Search completed: July 16, 2004, 00:03:55  
Job time : 66.5401 secs



Result No.	Score	Query Match	Length	DB	ID	Description	
1	429	28.2	299	2	S56749	functional adhesio	
2	201.5	13.2	2	2	JC7780	coxsackie- and ade	
3	186	12.2	811	2	A41054	fasciclin II, tran	
4	186	12.2	873	2	B41054	fasciclin II, PI-II	
5	171	11.2	6642	2	T29757	protein UNC-89 - C	
6	163.5	10.7	7962	2	I39346	elastic titin - hu	
7	160.5	10.6	1367	2	A41228	protein-tyrosine k	
8	157	10.3	344	2	A27681	nonspecific cross-	
9	157	10.3	860	2	JC5702	Erbb kinase activa	
10	157	10.3	858	2	JC5701	Erbb kinase activa	
11	156	10.3	1897	1	TDHULK	leukocyte antigen	
12	155.5	10.2	1328	2	T23007	hypothetical prote	
13	155.5	10.2	2783	2	T34416	hypothetical prote	
14	155	10.2	725	2	JE0100	neural cell adhesi	
15	155	10.2	850	2	JC5700	Erbb kinase activa	
16	153.5	10.1	521	2	JC1508	biliary glycoprote	
17	152	10.0	773	2	T46283	hypothetical prote	
18	152	10.0	5175	2	T20992	hypothetical prote	
19	152	10.0	5198	2	T43590	hemiscitin precurs	
20	151.5	10.0	1033	2	S19247	cell adhesion prot	
21	151	9.9	1092	1	JN0635	neural cell adhesi	
22	151	9.9	1501	2	I58148	protein-tyrosine-p	
23	151	9.9	1863	2	S46217	protein-tyrosine-p	
24	151	9.9	1898	2	S46216	leukocyte antigen-	
25	150.5	9.9	521	2	S43338	biliary glycoprote	
26	150	9.9	1499	2	I50212	protein-tyrosine-p	
27	150	9.9	1907	2	S50893	protein-tyrosine-p	
28	149.5	9.8	352	2	T33433	hypothetical prote	
29	148.5	9.8	519	2	A44783	ecto-ATPase precu	

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Db      233 ERNVGVIVAALVTLILLGILVFGIWFAYSRGHFDRT---KKGTSSKKVIYSQPSARSEG 289
QY      289 DPKHTYSFII 298
          :||| :||| :
Db      290 EFKQTSSFLV 299

RESULT 2
JC7780
cox sackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7780
R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-references: GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match      13.2%; Score 201.5; DB 2; Length 365;
Best Local Similarity 24.5%; Pred. No. 1.2e-08;
Matches 78; Conservative 46; Mismatches 130; Indels 65; Gaps 11;

QY      12 LLRLVVALGVHKAAGSAPKQOVTVAVXQEAIIACK---TFKTVXSRLSEW----- 63
Db      3 LLRLFLLCGVADFTRGISITTPBQMIEKAGETAYLPCKFTLPGDEGPDIDIELLSIPA 62

QY      64 --KKI-----GRSVFVYVYQOTLOGDFKNRAEMI-----DFNIRIKNVTRSDAGK 106
Db      63 DNQKVDQVILLYSGDKIYDDYQ-----DLKGRVFTSNLKGSGDASINVTNLQSLDGT 117

QY      107 YRCEV-SAPSEOGQNLBEDTVILEVLVAPVSPSEVPSSALSGLGVVELRCODKSGNPAPE 165
Db      118 YQCKVKAPGVGNKKIQ-----LTVLRPSGIRCYVDGSEBIGNDFLKCPEKSGSLPLR 172

QY      166 YWFWDGIRLLENPRLGQSSTNSYTMNTKTGTQFNVTSKLDTGECSEARNVSGVRRRC 225
Db      173 YEWQK-----LSDQKLPISLWPEMTSPVISVKNASAEYSGTYTCTVRNVGSDQC 223

QY      226 -----PGKMQVDDLNISGIIAAVVVALVSVGLGVCYAQRKGYSKETSFO--- 274
Db      224 LLRLDVPFPPSNRAGTIAGAVIGTLLALVLIALLIVFCCH-----KKRREEKYEYVHHDIR 279

QY      275 -----KSNSSSKATTMSEN 288
Db      280 DVPPPKSRTSTARSVIGSN 298

RESULT 3
A41054
fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: A41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: A41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-811 <GRE>
A:Cross-references: GB:M77165; NID:g157402; PID:g157403
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-references: FlyBase: FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: membrane protein

Query Match      12.2%; Score 186; DB 2; Length 811;
Best Local Similarity 24.6%; Pred. No. 6e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY      30 SAPKQOVTVAVXQEAIIACKT---PKKTVXSRLSEWKLK---BSVSFVYVYQOTLOGDF 83
Db      142 NAPENQYPTLG---QDYVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVQT----- 189

QY      84 KRAEMIDFNIRIKNVTRSDAGKYRCEVSPSEOGQNLBEDTVILEVLVAPVSPSEVP 143
Db      190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY      144 SALSGLTVELRCODKEGNPAPEYTFWKDGIIRLLENPRLGQSSTNSYTMNTKTGTQLQNT 203
Db      240 EAVEGKFPFAANCTAR-GKVPVPEISMIRDATQL-----NVATADRFOVNPOTGLVTISS 291

QY      204 VSKLDTGEYSCBARNVSGVRRCPGK-----RMQVDDL-NISGIIAAVVVALVSVCGLG 257
Db      292 VSQDDYGTVTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY      258 VCYAQRKGYSKETSFOKSNSSSKATTMSEND 289
Db      342 TCRA--KGRPAPAITFRRWGTQEYVINGQDD 371

RESULT 4
B41054
fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: B41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: B41054
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-873 <GRE>
A:Cross-references: GB:M77166
C:Genetics:
A:Gene: FlyBase: Fas2
A:Cross-references: FlyBase: FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C:Keywords: transmembrane protein

Query Match      12.2%; Score 186; DB 2; Length 873;
Best Local Similarity 24.6%; Pred. No. 6e-07;
Matches 67; Conservative 50; Mismatches 101; Indels 54; Gaps 13;

QY      30 SAPKQOVTVAVXQEAIIACKT---PKKTVXSRLSEWKLK---BSVSFVYVYQOTLOGDF 83
Db      142 NAPENQYPTLG---QDYVMCEVKADPNPTI---DWLRNGDPITRTNDKYVVQT----- 189

QY      84 KRAEMIDFNIRIKNVTRSDAGKYRCEVSPSEOGQNLBEDTVILEVLVAPVSPSEVP 143
Db      190 -----NGLLRNVQESDEGIYTCR-AAVETGELLER-TIRVEVFIQPEIISLPTNL 239

QY      144 SALSGLTVELRCODKEGNPAPEYTFWKDGIIRLLENPRLGQSSTNSYTMNTKTGTQLQNT 203
Db      240 EAVEGKFPFAANCTAR-GKVPVPEISMIRDATQL-----NVATADRFOVNPOTGLVTISS 291

QY      204 VSKLDTGEYSCBARNVSGVRRCPGK-----RMQVDDL-NISGIIAAVVVALVSVCGLG 257
Db      292 VSQDDYGTVTCLAKNRAGVVDQTKLNLVLRPQIYELYNVTGARTKEIAI----- 341

QY      258 VCYAQRKGYSKETSFOKSNSSSKATTMSEND 289
Db      342 TCRA--KGRPAPAITFRRWGTQEYVINGQDD 371

RESULT 5

```



## RESULT 8

A27681  
non-specific cross-reacting antigen precursor - human  
N:Alternate names: NCA; TEX/NCA  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 31-Jan-2000  
C:Accession: A26902; A29875; A27661; B31037; A29918; A27709; A36271; C26414; E44476; F44  
R:Oikawa, S.; Kosaki, G.; Nakazato, H.  
Biochem. Biophys. Res. Commun. 146, 464-469, 1987  
A:Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene  
A:Reference number: A26902; MUID:87298464; PMID:3619891  
A:Accession: A26902  
A:Molecule type: DNA  
A:Residues: 1-141 <OI>  
A:Cross-references: GB:M17082; NID:gl80230; PIDN:AAA51971.1; PID:9553222  
R:RThompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2365-2369, 1987  
A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene family  
A:Reference number: A29875; MUID:87204248; PMID:3033672  
A:Accession: A29875  
A:Molecule type: DNA  
A:Residues: 23-141 <THO>  
A:Cross-references: GB:M15337  
A:Note: the authors translated the codon ACT for residue 64 as Tyr  
R:Ritawagi, Y.; Oikawa, S.; Matsuo, Y.; Kosaki, G.; Nakazato, H.  
Biochem. Biophys. Res. Commun. 150, 89-96, 1988  
A:Title: Primary structure of non-specific cross-reacting antigen (NCA), a member of carcinoembryonic antigen (CEA) gene family  
A:Reference number: A27681; MUID:88106638; PMID:3337731  
A:Accession: A27681  
A:Molecule type: mRNA  
A:Residues: 1-238, 'V', 240-344 <TAW>  
A:Cross-references: GB:M18728; NID:gl89084; PIDN:AAA59907.1; PID:gl89085  
R:RBarrett, T.; Goebel, S.J.; Notthardt, M.A.; Elting, J.J.  
Genomics 3, 59-66, 1988  
A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA  
A:Reference number: A31037; MUID:89122014; PMID:3220478  
A:Accession: B31037  
A:Molecule type: mRNA  
A:Residues: 1-137, 'L', 139-344 <BAR>  
A:Cross-references: GB:M29541; NID:gl89103; PIDN:AAA59915.1; PID:gl89104  
A:Note: the authors translated the codon TTG for residue 138 as Phe  
R:RNeumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.  
J. Biol. Chem. 263, 3202-3207, 1988  
A:Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (NCA)  
A:Reference number: A29918; MUID:88139389; PMID:2830274  
A:Accession: A29918  
A:Molecule type: mRNA  
A:Residues: 1-344 <NEU>  
A:Cross-references: GB:M18216; GB:J03550; NID:gl78690; PIDN:AAA51739.1; PID:gl78691  
R:RGrunert, F.; Kolbinger, F.; Schwarz, K.; Schwaiblmair, H.; von Kleist, S.  
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988  
A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and indicates a distinct glycoform  
A:Reference number: A27709; MUID:88268882; PMID:3390172  
A:Accession: A27709  
A:Molecule type: protein  
A:Residues: 35-95; 99-120; 123-138; 143-151, 'X', 153-162; 166, 'X', 168-172, 'X', 174-193; 231-235  
R:RHeita, S.A.; Paxton, R.J.; Shively, J.E.  
J. Biol. Chem. 265, 8618-8626, 1990  
A:Title: Sequence and glycosylation site identity of two distinct glycoforms of non-specific cross-reacting antigen (NCA)  
A:Reference number: A36271; MUID:90256782; PMID:2341397  
A:Accession: A36271  
A:Molecule type: protein  
A:Residues: 35-42; 44-53; 55-80; 83-134; 139-160; 166-172; 174-180; 191-194; 204-224; 233-308; 310  
R:Paxton, R.J.; Mosser, G.; Pande, H.; Lee, T.D.; Shively, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987  
A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation sites  
A:Reference number: A26414; MUID:87147209; PMID:3469650  
A:Accession: C26414  
A:Molecule type: protein  
A:Residues: 35-69 <PAX>  
R:R.Khan, W.N.; Praeger-Gyarmay, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.  
Genomics 14, 384-390, 1992  
A:Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen (CEA) gene family





submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19651

A:Accession: T23007  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
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A:Cross-references: EMBL:Z68005; PIDN:CAA91994.1; GSPDB:GN00028; CESP:K09C8.5  
A:Experimental source: Clone F59F3  
R:Kershaw, J.

submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19755

A:Accession: T23543  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1328 <WIL>  
A:Cross-references: EMBL:Z68006; PIDN:CAA91999.1; GSPDB:GN00028; CESP:K09C8.5  
A:Experimental source: clone K09C8  
C:Genetics:  
A:Gene: CESP:K09C8.5  
A:Map position: X  
A:Introns: 34/1, 85/3; 133/3; 182/2; 220/3; 262/2; 390/3; 442/2; 493/3; 563/2; 586/3; 61

Query Match 10.2%; Score 155.5; DB 2; Length 1328;

Best Local Similarity 27.5%; Pred. No. 0.00028;  
Matches 42; Conservative 34; Mismatches 66; Indels 11; Gaps 4;

Db 69 SVSFVYVQOTLQGFKNFAEMIDFNIRKNTSDAGKYRCEVSAPEQGNLEEDTVTL 128

Db 382 TITWLFPEKQKTESKHLTKNGSVLKLFPPLNTDIGQYECVANGESKSHI--FSVSL 439

Qy 129 EVLVAPVSPCEVPSSALSGTWELRCQKGNPAPYTWFKDGIRLLENPRLGQSQTNS 188

Db 440 KESEQVPIIDAPMDTNATIGQQVTLRCNAK-GFFVPDVVWLFEGIRI--PR-----RNT 490

Qy 189 SYTWNTKTGTQFNVTSKLDTGEVSCARNVSG 221

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

Db 491 RYTISSNNIEITIEKVTNRHDSGVFTCAVNSVG 523

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Qy 243 AVVVVALVTSV 253

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Query Match  
10.2%; Score 155; DB 2; Length 850;

Query Match	10.2%;	Score 155;	DB 2;	Length 850;
Best Local Similarity	27.7%;	Pred. No. 0.00018;		
Matches 56;	Conservative 24;	Mismatches 86;	Indels 36;	Gaps 8;

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V  
W  
X  
Y  
Z

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QY  
637 GATTAAAAATTAACCTACT 290

DD 340 GHARACNEIARSICVNG-GVCI 360

Search completed: July 15, 2004, 23:55:07  
Job time : 24.3102 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:03 ; Search time 12.7487 Seconds  
(without alignments)  
1217.140 Million cell updates/sec

Title: US-09-852-797-76  
Perfect score: 1521  
Sequence: 1 MARRSRHRLLLRLYLVA.....SSKATMSSEDFKTKSFII 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1518	99.8	298	JAM2_HUMAN	P57087 homo sapien
2	429	28.2	299	JAM1_HUMAN	O9Y624 homo sapien
3	421	27.7	300	JAM1_MOUSE	O88792 mus musculu
4	415.5	27.3	298	JAM1_BOVIN	Q9X556 bos taurus
5	231	15.2	319	A33_HUMAN	Q99795 homo sapien
6	195.5	12.9	365	CXAR_HUMAN	P78110 homo sapien
7	186	12.2	873	FAS2_DROME	P34082 drosophila
8	180	11.8	365	CXAR_MOUSE	P97792 mus musculu
9	171	11.2	632	UN89_CABEL	O01761 caenorhabdi
10	164	10.8	344	CEA8_HUMAN	P40199 homo sapien
11	160.5	10.6	1367	VGR2_MOUSE	P35918 mus musculu
12	159.5	10.5	837	NMG2_MOUSE	O35136 mus musculu
13	157	10.3	868	NRG2_RAT	O35569 rattus norv
14	156	10.3	756	NRG2_MOUSE	P56974 mus musculu
15	155	10.3	1897	PTPF_HUMAN	P10586 homo sapien
16	155.5	10.2	837	NMG2_HUMAN	O15394 homo sapien
17	155	10.2	850	NRG2_HUMAN	O14511 homo sapien
18	153.5	10.1	521	CEA1_MOUSE	P31809 mus musculu
19	153.5	10.1	1343	VGR2_RAT	O08775 rattus norv
20	151	9.9	1092	NCA2_XENLA	P36335 xenopus lae
21	148.5	9.8	519	ECTO_RAT	P16573 rattus norv
22	148	9.7	1088	NCA1_XENLA	P16170 xenopus lae
23	148	9.7	1277	CAM1_FUGRU	O98902 fuigu rubrip
24	147.5	9.7	1091	NCA1_CHICK	P23550 gallus gall
25	147.5	9.7	1091	PTPD_HUMAN	P23468 homo sapien
26	147	9.7	526	CEA1_HUMAN	P13688 homo sapien
27	146.5	9.6	761	NCA2_HUMAN	P13592 homo sapien
28	146.5	9.6	848	NCA1_HUMAN	P13591 homo sapien
29	145	9.6	1051	PTK7_CHICK	O91048 gallus gall
30	145	9.5	333	AMAL_DROME	P15364 drosophila
31	145	9.5	764	ITCCN_DROME	Q08180 drosophila
32	145	9.5	1302	NRG_DROME	P20241 drosophila
33	144.5	9.5	349	CEA8_HUMAN	P31957 homo sapien

34	143.5	9.4	1948	1	PTNS_HUMAN	Q13332 homo sapien
35	143	9.4	858	1	NCA1_RAT	P13596 rattus norv
36	142.5	9.4	265	1	CEA7_HUMAN	Q14002 homo sapien
37	140.5	9.2	344	1	NTRI_RAT	Q82718 rattus norv
38	140.5	9.2	847	1	CD22_HUMAN	P20273 homo sapien
39	140	9.2	359	1	LACH_DROME	Q24372 drosophila
40	140	9.2	853	1	NCA1_BOVIN	P18336 bos taurus
41	140	9.2	1906	1	KMLS_CHICK	P11799 gallus gall
42	140	9.2	4391	1	PGBM_HUMAN	P98160 homo sapien
43	139	9.1	725	1	NCA2_MOUSE	P13594 mus musculu
44	139	9.1	1115	1	NCA1_MOUSE	P13595 mus musculu
45	139	9.1	3707	1	PGBM_MOUSE	Q05793 mus musculu

ALIGNMENTS

RESULT 1  
JAM2\_HUMAN  
ID JAM2\_HUMAN STANDARD; PRT; 298 AA.  
AC P57087;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Junctional adhesion molecule 2 precursor (Vascular endothelial  
DE Junction-associated molecule) (VE-JAM).  
GN JAM2 OR VEJAM OR C21ORF43.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vascular endothelial cells;  
RX MEDLINE=20317114; PubMed=10779521;  
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;  
RT "Vascular endothelial junction-associated molecule, a novel member of  
RT the immunoglobulin superfamily, is localized to intercellular  
RT boundaries of endothelial cells.";  
RL J. Biol. Chem. 275:19139-19145(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=20507930; PubMed=10945976;  
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,  
RT "A novel protein with homology to the junctional adhesion molecule:  
RT Characterization of leukocyte interactions.";  
RL J. Biol. Chem. 275:34750-34756(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

web data

CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO  
 CC SECONDARY LYMPHOID ORGANS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL  
 CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.  
 CC CELLULARIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL  
 CC CELLS.  
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3 (2001);  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1652492186.g.htm".  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF255910; AAF81223.1; -;  
 CC EMBL; AY016009; AAG49022.1; -;  
 CC EMBL; BC017779; AAH17779.1; -;  
 CC Genbank; HGNC:14686; JAM2.  
 CC MIM; 606870; -;  
 CC GO; GO:0005887; C: integral to plasma membrane; NAS.  
 CC GO; GO:0016337; P: cell-cell adhesion; NAS.  
 CC InterPro; IPR007110; IG-like.  
 CC InterPro; IPR003598; IG\_c2.  
 CC Pfam; PF00047; IG; 2.  
 CC SMART; SM00408; IGC2; 1.  
 CC PROSITE; PS50835; IG\_LIKE; 2.  
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  
 CC SIGNAL 1 20 POTENTIAL.  
 CC CHAIN 21 298 JUNCTIONAL ADHESION MOLECULE 2.  
 CC DOMAIN 21 238 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 239 259 POTENTIAL.  
 CC DOMAIN 260 298 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 32 127 IG-LIKE V-TYPE.  
 CC DOMAIN 134 238 IG-LIKE C2-TYPE.  
 CC DOMAIN 150 109 POTENTIAL.  
 CC DISULFID 155 214 POTENTIAL.  
 CC CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 Best Local Similarity 99.3%; Pred. No. 5.8e-121;  
 Matches 296; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 Db 1 MARSRRLLRLLLRLYLVALGYHKGYSAPKDDQVVTAVYQEAAILACKTKPKTVXSR 60  
 Qy 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRKNVTRSDAGKYRCEVSPSQGN 120  
 Db 61 LEWKLGSRVSFVYQOTLQDGFKNRAEMIDFNIRKNVTRSDAGKYRCEVSPSQGN 120  
 Qy 121 LEEDTVTLVLVAVPVCSEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRLLLENPR 180  
 Db 121 LEEDTVTLVLVAVPVCSEVPSSALSGTVVLRCDKEGNPAPEYTWFKDGRLLLENPR 180  
 Qy 181 LGSQSTNSSTYMTNKTGTLQFNVTSLDTCGEYSCARPNSVGYRCRCRQMQVDLINSIGI 240  
 Db 181 LGSQSTNSSTYMTNKTGTLQFNVTSLDTCGEYSCARPNSVGYRCRCRQMQVDLINSIGI 240  
 Qy 241 IAAVVVALVISVGLGVCAQKGYFSEKTSFKQNSSSSKATMTSENDFKHTKSFII 298  
 Db 241 IAAVVVALVISVGLGVCAQKGYFSEKTSFKQNSSSSKATMTSENDFKHTKSFII 298

RESULT 2  
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 ID JAM1\_HUMAN STANDARD; PRT; 299 AA.  
 AC Q9Y624;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE JUNCTIONAL adhesion molecule 1 precursor (JAM) (Platelet adhesion  
 DE molecule 1) (PAM-1) (Platelet FII receptor) (UNQ264/PRO301).  
 GN FII OR JAM1 OR JCAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 OX [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=99323940; PubMed=10395639;  
 RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,  
 RA Iwamatsu A., Kita T.;  
 RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution  
 RT of junctional adhesion molecule in human endothelial cells.";  
 RL J. Immunol. 163:553-557(1999).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RX Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,  
 RA Kornecki E.;  
 RT "Molecular cloning and sequencing of the cDNA of FII receptor, a  
 RT novel Ig superfamily member from human platelets";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 SEQUENCE FROM N.A.  
 RA Naik U.P., Naik M.U., DeLeon P., Spychala J.;  
 RT "Cloning and characterization of PAM-1, a novel platelet adhesion  
 RT molecule involved in platelet activation.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 SEQUENCE FROM N.A.  
 RX TISSUE=Brain;  
 MEDLINE=21154917; PubMed=11230166;  
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,  
 RA Lauber J., Dueterhoeft A., Beyer A., Koehler K., Strack N.,  
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Poustka A.;  
 RT "Towards a catalog of human genes and proteins: sequencing and  
 RT analysis of 500 novel complete protein coding human cDNAs.";  
 RL Genome Res. 11:422-435(2001).  
 RN [5]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=22887236; PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Sesagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandell R., Watanabe C., Wiesand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [6]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Scheetz T.B.,



```

CC CC interaction.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC CC Localized at tight junctions of both epithelial and endothelial
CC CC cells.
CC CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC CC epithelial and endothelial cells.
CC CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; U89915; AAC32982.1; -.
CC CC PDB; 1F97; 22-AUG-01.
CC CC MGD; MGI:1321398; F11r.
CC CC CO; CO:0005515; F:protein binding; IPI.
CC CC InterPro; IPR007110; IG-like.
CC CC Pfam; PF00047; IG_2.
CC CC SMART; SM00406; IGV; 1.
CC CC PROSITE; PS50835; IG LIKE; 2.
CC CC KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC CC Repeat; Signal; 3D-structure.
CC CC -----
CC CC SIGNAL 1 26 POTENTIAL.
CC CC CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
CC CC DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 239 259 POTENTIAL.
CC CC DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
CC CC DOMAIN 28 122 IG-LOPE V-TYPE 1.
CC CC DOMAIN 134 230 IG-LIKE V-TYPE 2.
CC CC DISULFID 49 108 POTENTIAL.
CC CC DISULFID 152 212 POTENTIAL.
CC CC CARBOHYD 42 42 N-LINKED (GLCNAC...) (POTENTIAL).
CC CC CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
CC CC SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97EC CRC64;
CC CC -----
Query Match 27.7%; Score 421; DB 1; Length 300;
Best Local Similarity 34.6%; Pred. No. 2.6e-28;
Matches: 104; Conservative 55; Mismatches 130; Indels 12; Gaps 6;
QY 4 RSRRLLLRLVVALGYHKAQVGFAPKQDQVTVAVYQEAALACKTPKTVXSRLW 63
DB 6 KAGKRLLEFLTSMILGSLVQKGSVYTAQSDVQYPE-----NESIKLTCTYSGFSSPVEW 61
QY 64 KKL-GRSVSVFYQOTLGGDFKNRAEMIDFNIRIKNTRSDAGKYREVSAPEQQGNLE 122
DB 62 KVVQGSTTALVCYNSQITAPVADRVTFFSSGKITPSSVTRKDNGETYTCWS--BEGGQNYG 119
QY 123 EDTVTLVLPVAPVPSCEPSSALSGTVLRLCODEKGNPAPEYTFKDGIRLLENPLRG 182
DB 120 EVSHLTVLVLPSPKPTISVSPSVTIGRAVLTCSEHDGSPSEYVSKDGLISMLTADAKX 179
QY 183 SQS--TNSYTNKTKTGLQFNVTSLKLDTGYSCEARNVSG-YRCPGKRVQVDLNLISGI 240
DB 180 TRAFMNSFTIDPKSGDLIFDPVTFAPDSGEVYCOAQNGYGTAVRSEAAHMDVAVELNVGGI 239
QY 241 IAAVVALVTVSVGLGVCAQRKGYE---SKETSFOKSNSSSKATWSENDFKTKSFI 297
DB 240 VAAVLVTLILGLLIFGWFAYSRGYFETTKKGTAPGKKVIYQSPTRSEGEFKQTSFL 299
QY 298 I 298
DB 300 V 300

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RESULT 4

JAMI\_BOVIN

ID JAMI\_BOVIN

STANDARD;

PRT; 298 AA.

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AC Q9XT56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN F11R OR JAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323940; PubMed=10395839;
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557(1999).
CC -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC formation. Appears early in primordial forms of cell junctions and
CC recruits PARD3. The association of the PARD6-PARD3 complex may
CC prevent the interaction of PARD3 with JAM1, thereby preventing
CC tight junction assembly (By similarity). Plays a role in
CC regulating monocyte transmigration involved in integrity of
CC epithelial barrier. Involved in platelet activation.
CC -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC association between PARD3 and PARD6B probably disrupts this
CC interaction (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AF111714; AA042051.1; -.
CC CC InterPro; IPR007110; IG-like.
CC CC Pfam; PF00047; IG_2.
CC CC SMART; SM00408; IGV; 2.
CC CC PROSITE; PS50835; IG LIKE; 2.
CC CC KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC CC Repeat; Signal.
CC CC -----
CC CC SIGNAL 1 24 POTENTIAL.
CC CC CHAIN 25 298 JUNCTIONAL ADHESION MOLECULE 1.
CC CC DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 238 258 POTENTIAL.
CC CC DOMAIN 239 298 CYTOPLASMIC (POTENTIAL).
CC CC DOMAIN 28 124 IG-LIKE V-TYPE 1.
CC CC DOMAIN 134 227 IG-LIKE V-TYPE 2.
CC CC DISULFID 49 108 POTENTIAL.
CC CC DISULFID 152 211 POTENTIAL.
CC CC CARBOHYD 184 184 N-LINKED (GLCNAC...) (POTENTIAL).
CC CC SEQUENCE 298 AA; 32456 MW; 714FE1C1714769A2 CRC64;
CC CC -----
Query Match 27.3%; Score 415.5; DB 1; Length 298;
Best Local Similarity 35.1%; Pred. No. 7.4e-28;
Matches 107; Conservative 47; Mismatches 118; Indels 33; Gaps 10;
QY 9 LLL---LLRLVVALGYHKAQVGFAPKQDQVTVAVYQEAALACKTPKTVXSRLW 60
DB 12 LLLFTSMILCSLALGRGAVQY-----EPVVRVPPNNPAKLSCSYSGFSSP-----R 58
QY 61 LEWK-KLGRSVSVFYQOTLGGDFKNRAEMIDFNIRIKNTRSDAGKYREVSAPEQQGNLE 119

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Db 59 VEWKFTGDIRGLVYNNKITASYENRVTFTDITGTFHVSRTKDTGMYTCMVS--DEGN 116
QY 120 NLEEDVTLEVLNAPVBSCEVPSSALSSTGVVELRCODKEGPAPEYTWFKDGRILLENP 179
Db 117 TYGEVTVQLVILVPPSKPTINPVSSVTIGTRAVLTCSEDRGPPPSYKWKFGVEMPLEP 176
QY 180 RLGSQSTNSYNTMTKTGLQFNTVSKLDTGEVSCFARNVSVYRCPGK---RMQVDDL 235
Db 177 KSNRAFSNSSLNTLQKGTGELIFDPVSASDTGDFTCQAN--GY-ASPVKSDTVHMDAVEL 233
QY 236 NISGITAANVVVALVSVCGLVGYCAQRKGYF--SKETSFKNSSSKATTSSENDPKHT 293
Db 234 NVGGIVAANFVTLILGALIFGWIFSRGYDFRANKGTSNKVIYSQPNARSDGFEFOT 293
QY 294 KSPII 298
Db 294 SSFLV 298

RESULT 5
A33_HUMAN
ID A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Colon carcinoma;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-P., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
POST-TRANSLATIONAL MODIFICATIONS.
RA MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC
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CC -----
CC EMBL; U79725; AAC50957.1; -.
CC Genew; HGNC:4445; GPA33.
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DR MIM; 602171; -.
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 235
FT TRANSMEM 236 256
FT DOMAIN 257 319
FT DOMAIN 22 134
FT DOMAIN 140 227
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 146 222
FT DISULFID 162 211
FT CARBOHYD 112 112
FT CARBOHYD 200 200
FT CARBOHYD 223 223
FT SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;
Query Match 15.2%; Score 231; DB 1; Length 319;
Best Local Similarity 28.6%; Pred. No. 3.1e-12; Indels 42; Gaps 11;
Matches 72; Conservative 41; Mismatches 97;
QY 30 SAPKQDVVAVXYQEAIALACKTPKTVXSR---LEWKKL-----GRSVSFVYQOT-LQ 80
Db 23 SVETPDVLRASQGSVTLPC-TYHTSTSSREGLIQWDKLLLTHTERVVWPFSSKNVIH 81
QY 81 GD-FKNR-----AEMDFNIRKNTVRSQDAGKRCFVSAPSEQQNLEEDT---VTLEV 130
Db 82 GELYKNRYSISNNAEQSDASITIDQLTMADNGTYECSVLSMSD----LEGNTKSRVLLV 137
QY 131 LVAPVPSCEVPSSALSQGVVELRCQDKGNPAPEYTWFKDGRILLENPRLGSGQSTNSSY 190
Db 138 LVPPKPECGTGETIIGNLTQCSKEGSTPTQYSWKRYNINLQEQPLAQPASGQPVSV 197
QY 191 TWNTKTGLQFNTVSKLDTGEVSCFARNVSVYRCP-GKRMQVDDLNIS-----GIA 242
Db 198 LKNISTDT-----SGYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAGVVA 247
QY 243 AVVVVALVSVIC 254
Db 248 ALIIIGIIYYCC 259

RESULT 6
CXAR_HUMAN
ID CXAR_HUMAN STANDARD; PRT; 365 AA.
AC P78310; O00694;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Brognoett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5."
RT Science 275:1320-1323(1997).
```

[2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97250541; PubMed=9096337;  
 RA Tomko R.P., Xu R., Philipson L.;  
 RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C  
 RT adenoviruses and group B coxsackieviruses";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20008750; PubMed=10543405;  
 RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,  
 RA Bowles N.E.;  
 RT "Genomic organization and chromosomal localization of the human  
 RT coxsackievirus B-adenovirus receptor gene";  
 RL Hum. Genet. 105:354-359(1999).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;  
 RA "Sequence and expression of CXADR, the human gene for the  
 RT coxsackievirus and adenovirus receptor";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX Anderson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalon D.K., Wozny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND  
 CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC  
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 CC  
 DR EMBL; Y07593; CAA68868.1; -;  
 DR EMBL; U0716; AAC51234.1; -;  
 DR EMBL; AF169366; AAF05908.1; -;  
 DR EMBL; AF169360; AAF05908.1; JOINED.  
 DR EMBL; AF169361; AAF05908.1; JOINED.  
 DR EMBL; AF169362; AAF05908.1; JOINED.  
 DR EMBL; AF169363; AAF05908.1; JOINED.  
 DR EMBL; AF169364; AAF05908.1; JOINED.  
 DR EMBL; AF169365; AAF05908.1; JOINED.

DR EMBL; AF200465; AAF24344.1; -;  
 DR EMBL; AF242865; AAG01088.1; -;  
 DR EMBL; AF242862; AAG01088.1; JOINED.  
 DR EMBL; AF242864; AAG01088.1; JOINED.  
 DR EMBL; BC003684; AAH03684.1; -;  
 DR EMBL; BC010536; AAH10536.1; -;  
 DR PDB; 1EAD; 13-JUL-01.  
 DR PDB; 1FSW; 08-NOV-99.  
 DR PDB; 1KAC; 24-NOV-99.  
 DR Genew; HGNC:2559; CXADR.  
 DR MIM; 602621; -;  
 DR GO; GO:0005887; C-integral to plasma membrane; TAS.  
 DR GO; GO:0004872; F-receptor activity; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS00835; IG-LIKE; 2.  
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Repeat; 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.  
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 20 134 IG-LIKE C2-TYPE 1.  
 FT DOMAIN 141 228 IG-LIKE C2-TYPE 2.  
 FT DISULFID 41 120 BY SIMILARITY.  
 FT DISULFID 162 212 BY SIMILARITY.  
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;  
 Query Match 12.9%; Score 195.5; DB 1; Length 365;  
 Best Local Similarity 23.3%; Pred. No. 3.6e-09;  
 Matches 67; Conservative 57; Mismatches 123; Indels 41; Gaps 9;  
 QY 10 LLLLLLYVALGVHKA YGFA PKDQVVAVVQVQVAILACK---TPKKT VXSRLW--- 63  
 Db 3 LLLCFVLLGVVDFARSLSIITP---EEMERAKGETALVLPCKFTLSPEQGLDLEWLIS 60  
 QY 64 ----KKLGRSVFVYQOTLQDF-----KRAEMIDFNIRKNTVRSAGKYR 108  
 Db 61 PADNOKVQD-VILYSGDKIYDVPDLKGRVHFTSNDLKSQDASINVTNLQSLDITGYQ 119  
 QY 109 CAVSAPSEQGNLEBDTIVLEVLNAPVPSCEVPSALSGLTVVELRCCKGNPAPEYTW 168  
 Db 120 CKV----KAPGVANKIHLVVLVPSGARCVDGSEIGSDFKIKCEPKGSLPQIEW 175  
 QY 169 FKDGIRLLENPLRGSQSTNSYTMNTKTGTLQFNVTSKLDTGEVSCSEARNVGVRRCPGK 228  
 Db 176 QK-----LSDSQKMTGWLAEHTSSVSVKSNASSEYSGTYSCTVVRNVGSDQCLLR 226  
 QY 229 RMQVDDLAISGLIIA-AVVVVALVSVCGVGYAQRKGYFSKETSFOK 275  
 Db 227 LNVPPSPNAGLIAGIIGTLIALALIGLIIFCCRKK---RREKYEK 271  
 RESULT 7  
 FAS2 DROME  
 ID FAS2 DROME STANDARD; PRT; 873 AA.  
 AC P34082; P34083; Q9W4M6;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE FAS2 OR EG:EG0007.3 OR CG3665.  
 GN FAS2 OR EG:EG0007.3 OR CG3665.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR LOCATION,  
 RP AND TISSUE SPECIFICITY.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=22005695; PubMed=1913818;  
 RA Greeningloh G., Rehm E.J., Goodman C.S.;  
 RT "Genetic analysis of growth cone guidance in *Drosophila*: fasciclin II  
 RT functions as a neuronal recognition molecule.";  
 RL Cell 67:45-57(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Fendell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke S., Davenport L.S., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Rosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleeb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas A., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP REVISIONS, AND ALTERNATIVE SPLICING.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.E.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Ceiniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review".  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [4]  
 RP SEQUENCE OF 22-873 FROM N.A.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=20196011; PubMed=10731137;  
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,  
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,  
 RA Minana B., Karatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,  
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,  
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,  
 RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,  
 RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,  
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
 RA Glover D.M.;  
 RT "From sequence to chromosome: the tip of the X chromosome of *D.*  
 RT *melanogaster*";  
 RL Science 287:2220-2222(2000).  
 CC -!- FUNCTION: Neuronal recognition molecule for the MPI axon pathway,  
 CC pathway recognition for axons during the development of nerve  
 CC fascicles  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
 CC attached to the membrane by a GPI-anchor (isoform 2).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Comment-Experimental confirmation may be lacking for some  
 CC isoforms:  
 CC Name=1; Synonyms=A, Membrane-linked;  
 CC IsoId=P34082-1; Sequence=Displayed;  
 CC Name=2; Synonyms=C, Phosphatidylinositol-linked;  
 CC IsoId=P34082-2; Sequence=VSP\_002508, VSP\_002509;  
 CC Name=3; Synonyms=B;  
 CC IsoId=P34082-3; Sequence=VSP\_002506, VSP\_002507;  
 CC -!- TISSUE SPECIFICITY: In embryos, both isoforms are initially  
 CC expressed on the surface of the axons in the MPI pathway and later  
 CC on several other longitudinal axon fascicles.  
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
 CC -!- SIMILARITY: Contains 5 fibronectin type III domains.  
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 CC -----  
 CC EMBL; M77165; AA28537.1; -;  
 CC EMBL; M77166; AA28538.1; -;  
 CC EMBL; AL033125; CAA21825.1; -;  
 CC EMBL; AE003430; AAF45925.2; -;  
 CC EMBL; AE003430; AAN09119.1; -;  
 CC EMBL; AL033125; CAA21826.1; -;  
 CC FIR; A41054; A41054.  
 CC FlyBase; FBgn000635; Fas2.  
 CC GO; GO:0005886; C:plasma membrane; IDA.  
 CC GO; GO:0007156; P:homophilic cell adhesion; IDA.  
 CC GO; GO:0007611; P:learning and/or memory; IMP.  
 CC GO; GO:0016319; P:muscle body development; IMP.  
 CC GO; GO:008038; P:neuronal cell recognition; IDA.  
 CC GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.  
 CC InterPro; IPR008957; FN-III-like.  
 CC InterPro; IPR003961; FN-III.  
 CC InterPro; IPR007110; IG-like.  
 CC Pfam; PF00041; fn3; 2.  
 CC Pfam; PF00047; ig; 5.  
 CC SMART; SM00060; FN3; 2.  
 CC SMART; SM00408; IGC2; 3.  
 CC PROSITE; PS50835; IG\_LIKE; 5.  
 CC Cell adhesion; Glycoprotein; Repeat; Alternative splicing;  
 CC Immunoglobulin domain; Transmembrane; GPI-anchor; Signal;  
 CC Neurogenesis.  
 KW SIGNA1 1 28 POTENTIAL.  
 KW CHAIN 29 873 FASCICLIN II.  
 KW DOMAIN 29 751 EXTRACELLULAR (POTENTIAL).  
 KW TRANSMEM 752 769 POTENTIAL.  
 KW DOMAIN 770 873 CYTOPLASMIC (POTENTIAL).  
 KW DOMAIN 31 131 IG-LIKE C2-TYPE 1.  
 KW DOMAIN 138 223 IG-LIKE C2-TYPE 2.  
 KW DOMAIN 230 318 IG-LIKE C2-TYPE 3.  
 KW DOMAIN 323 423 IG-LIKE C2-TYPE 4.  
 KW DOMAIN 428 520 IG-LIKE C2-TYPE 5.  
 KW DOMAIN 544 619 FIBRONECTIN TYPE-III 1.



```
QY 186 SSVYMT-----KTGTLQNTVSKLDTGYSCARNVGVRCPCGKRMVDNLISGII 241
DQ 180 DSQTMPTPLAETSPVISVKNASSEYSGYSCVQNRVSDQOMLRDLVPPSNAGII 239
QY 242 AAVVV-----VALVISVCGLGVCYACR-----XGYFSKETSFOKSN 278
DQ 240 AGAVIGTLLALVLIGALFCCHRRKREKVEVHHDIREDVPPKSRRTSTARSYIGSNH 299
QY 279 SSKATTMSENDFKHTKS 295
DQ 300 SSLGMSNFSNMEGYSKT 316

RESULT 9
UN89 CAEL STANDARD; PRT; 6632 AA.
AC 001761; Q17362;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
GN UNC-89 OR COSD1.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=Bristol N2; PubMed=8603916;
RX MEDLINE=96180278;
RA Benian G.M., Tinley T.B., Tang X., Borodovsky M.;
RT "The Caenorhabditis elegans gene unc-89, required for muscle M-line
RT assembly, encodes a giant modular protein composed of Ig and signal
RT transduction domains.";
RL J. Cell Biol. 132:835-848(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Le T.T., Wilson R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
REVIEWS.
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Structural component of the muscle M-line. Myofilament
CC lattice assembly begins with positional cues laid down in the
CC basement membrane and muscle cell membrane. UNC-89 responds to
CC these signals, localizes, and then participates in assembling an
CC M-line.
CC -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
CC -!- SIMILARITY: Contains 1 DEL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 5 RCSD domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
CC EMBL; U33058; AAB0542.1; -.
CC EMBL; AF003131; AAB54132.2; -.
CC PDB; 1FHO; 20-DEC-00.
CC WormPep; C09D1.1; CB30426.
CC InterPro; IPR008957; FN.III-like.
CC InterPro; IPR003961; FN.III.
CC InterPro; IPR007110; IG-like.
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DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR001849; PH.
DR InterPro; IPR007850; RCSD.
DR InterPro; IPR000219; RHOGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 47.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF05177; RCSD; 5.
DR Pfam; PF06211; RHOGEF; 1.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00408; IGC2; 23.
DR SMART; SM00325; RHOGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50835; IG-LIKE; 49.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW Muscle protein; immunoglobulin domain; Repeat; SH3 domain;
KW 3D-structure.
FT DOMAIN 63 127 SH3.
FT DOMAIN 152 330 DH.
FT DOMAIN 342 438 PH.
FT DOMAIN 547 633 IG-LIKE C2-TYPE 1.
FT DOMAIN 648 736 IG-LIKE C2-TYPE 2.
FT DOMAIN 748 838 IG-LIKE C2-TYPE 3.
FT DOMAIN 946 1033 IG-LIKE C2-TYPE 4.
FT DOMAIN 1044 1132 IG-LIKE C2-TYPE 5.
FT DOMAIN 1140 1227 IG-LIKE C2-TYPE 6.
FT DOMAIN 1272 1315 THR-RICH.
FT DOMAIN 1375 1475 RCSD 1.
FT DOMAIN 1479 1585 RCSD 2.
FT DOMAIN 1597 1695 RCSD 3.
FT DOMAIN 1700 1799 RCSD 4.
FT DOMAIN 1800 1860 RCSD 5.
FT DOMAIN 1982 2067 IG-LIKE C2-TYPE 7.
FT DOMAIN 2071 2163 IG-LIKE C2-TYPE 8.
FT DOMAIN 2171 2281 IG-LIKE C2-TYPE 9.
FT DOMAIN 2269 2359 IG-LIKE C2-TYPE 10.
FT DOMAIN 2367 2455 IG-LIKE C2-TYPE 11.
FT DOMAIN 2463 2564 IG-LIKE C2-TYPE 12.
FT DOMAIN 2563 2651 IG-LIKE C2-TYPE 13.
FT DOMAIN 2657 2746 IG-LIKE C2-TYPE 14.
FT DOMAIN 2754 2858 IG-LIKE C2-TYPE 15.
FT DOMAIN 2887 2980 IG-LIKE C2-TYPE 16.
FT DOMAIN 2994 3081 IG-LIKE C2-TYPE 17.
FT DOMAIN 3087 3183 IG-LIKE C2-TYPE 18.
FT DOMAIN 3189 3280 IG-LIKE C2-TYPE 19.
FT DOMAIN 3286 3376 IG-LIKE C2-TYPE 20.
FT DOMAIN 3384 3469 IG-LIKE C2-TYPE 21.
FT DOMAIN 3482 3572 IG-LIKE C2-TYPE 22.
FT DOMAIN 3580 3667 IG-LIKE C2-TYPE 23.
FT DOMAIN 3686 3777 IG-LIKE C2-TYPE 24.
FT DOMAIN 3817 3908 IG-LIKE C2-TYPE 25.
FT DOMAIN 3920 4009 IG-LIKE C2-TYPE 26.
FT DOMAIN 4018 4106 IG-LIKE C2-TYPE 27.
FT DOMAIN 4109 4201 IG-LIKE C2-TYPE 28.
FT DOMAIN 4212 4287 IG-LIKE C2-TYPE 29.
FT DOMAIN 4302 4387 IG-LIKE C2-TYPE 30.
FT DOMAIN 4400 4485 IG-LIKE C2-TYPE 31.
FT DOMAIN 4489 4580 IG-LIKE C2-TYPE 32.
FT DOMAIN 4588 4678 IG-LIKE C2-TYPE 33.
FT DOMAIN 4681 4771 IG-LIKE C2-TYPE 34.
FT DOMAIN 4873 4961 IG-LIKE C2-TYPE 35.
FT DOMAIN 4965 5057 IG-LIKE C2-TYPE 36.
FT DOMAIN 5067 5160 IG-LIKE C2-TYPE 37.
FT DOMAIN 5171 5260 IG-LIKE C2-TYPE 38.
FT DOMAIN 5277 5366 IG-LIKE C2-TYPE 39.
FT DOMAIN 5383 5472 IG-LIKE C2-TYPE 40.
FT DOMAIN 5487 5578 IG-LIKE C2-TYPE 41.
FT DOMAIN 5595 5685 IG-LIKE C2-TYPE 42.
FT DOMAIN 5701 5790 IG-LIKE C2-TYPE 43.
```

FT DOMAIN 5815 5904  
 FT DOMAIN 5925 6014  
 FT DOMAIN 6038 6130  
 FT DOMAIN 6150 6239  
 FT DOMAIN 6275 6368  
 FT DOMAIN 6413 6502  
 FT DOMAIN 6507 6596  
 FT DISULFID 568 621  
 FT DISULFID 2908 2975  
 FT DISULFID 3015 3065  
 FT DISULFID 3707 3759  
 FT DISULFID 3826 3890  
 FT DISULFID 5092 5157  
 FT DISULFID 5298 5350  
 FT DISULFID 5508 5560  
 FT DISULFID 5616 5669  
 FT DISULFID 5722 5764  
 FT DISULFID 5836 5901  
 FT DISULFID 5946 5998  
 FT DISULFID 6036 6171  
 FT DISULFID 6421 6486  
 FT CONFLICT 2137 2137  
 FT CONFLICT 2245 2247  
 FT CONFLICT 2258 2258  
 FT CONFLICT 2284 2284  
 FT CONFLICT 2297 2297  
 FT CONFLICT 3531 3531  
 FT CONFLICT 3684 3688  
 FT CONFLICT 3929 3929  
 FT CONFLICT 5134 5134  
 FT CONFLICT 5145 5145  
 FT CONFLICT 5185 5185  
 FT CONFLICT 5199 5199  
 FT CONFLICT 5202 5202  
 FT CONFLICT 5213 5213  
 FT CONFLICT 6178 6178  
 FT CONFLICT 6268 6268  
 SQ SEQUENCE 6632 AA; 731665 MW; 262D3EDD62960E89 CRC64;  
 Query Match 11.2%; Score 171; DB 1; Length 6632;  
 Best Local Similarity 28.1%; Pred No. 1.5e-05;  
 Matches 61; Conservative 29; Mismatches 75; Indels 52; Gaps 11;  
 QY 28 GFSA PKDQV---TAVYQBAIIACKTPKTVXSRLEWKLGRSVFYVYQTFLOGDFK 84  
 Db 3813 GRGAEFVELLSCTVTKEQAILCKV-KGEPRPKWTKGKGVEM-----SAR 3862  
 QY 85 NRAEMID---FNIRIKNVTSDAGKYCEVSAPEQCNLEEDVTILEVLVAPVPSCEV 141  
 Db 3863 VRAEHKDDGTTLTFDNTQADAGEYRCE--AENEYGSANTGEGIIVTLGAPKIDG-EA 3919  
 QY 142 P-----SSALSGTVVELRCQKGNPAPEYTWFKDGRLLLENPLRGLSQST 186  
 Db 3920 PDFLQPKVPVTVGCTAVLEGKI-----SGKPKPSVKWYKNGEELKPSDRVKIE-- 3969  
 QY 187 NSSYMTNKTGTLPN-TVSKL-DTGEYSCEARNVG 221  
 Db 3970 -----NLDGDTQRLTITVNAKLDMDVEYRCASNEFG 4000

# RESULT 10 CEA6 HUMAN

ID CEA6 HUMAN STANDARD; PRT; 344 AA.  
 AC P40199; Q14920;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Carcinoembryonic antigen-related cell adhesion molecule 6 precursor  
 DE (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)  
 DE (CD66c antigen).  
 GN CEA6 OR NCA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89122014; PubMed=3220478;  
 RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;  
 RT "Carcinoembryonic antigen family: characterization of cDNAs coding  
 for NCA and CEA and suggestion of nonrandom sequence variation in  
 their conserved loop-domains";  
 RL Genomics 3:59-66(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Lung carcinoma;  
 RA MEDLINE=88106638; PubMed=3337731;  
 RA Tawaragi Y., Oikawa S., Matsuoka Y., Kosaki G., Nakazato H.;  
 RT "Primary structure of nonspecific crossreacting antigen (NCA), a  
 member of carcinoembryonic antigen (CEA) gene family, deduced from  
 cDNA sequence";  
 RL Biochem. Biophys. Res. Commun. 150:89-96(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Pancreas;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesberg R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -!- DATABASE: NCBIPROV; NOTE=CD guide CD66c entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd66c.htm".  
 CC -----  
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 CC -----  
 CC EMBL; M29541; AAA59915.1; -;  
 CC EMBL; M18728; AAA59907.1; -;  
 CC EMBL; BC005008; AAH05008.1; -;  
 CC Genew; HGNC:1818; CEACAM6.  
 CC MIM; 163980; -;  
 CC DR GO; 0005887; C:integral to plasma membrane; TAS.  
 CC DR GO; 0007267; P:cell-cell signaling; TAS.  
 CC DR GO; 0007165; P:signal transduction; TAS.  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003598; Ig\_c2.  
 CC DR Pfam; PF00047; Ig\_3.  
 CC DR SMART; SM00408; IGC2; 1.  
 CC DR PROSITE; PS50835; IG\_LIKE; 2.  
 CC DR Immunoglobulin domain; Antigen; Signal; Glycoprotein; GPI-anchor;  
 CC Repeat; Lipoprotein.





DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.  
 KW Angiogenesis; Signal; Transferase; Tyrosine-protein kinase; Receptor;  
 KW Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;  
 KW Immunoglobulin domain; Repeat  
 FT SIGNAL 1 19  
 FT CHAIN 20 1367  
 FT  
 FT DOMAIN 20 762  
 FT TRANSMEM 763 784  
 FT DOMAIN 785 1367  
 FT  
 FT DOMAIN 46 111  
 FT DOMAIN 143 209  
 FT DOMAIN 226 325  
 FT DOMAIN 330 416  
 FT DOMAIN 423 542  
 FT DOMAIN 549 656  
 FT DOMAIN 665 751  
 FT DOMAIN 832 1160  
 FT NP\_BIND 838 846  
 FT BINDING 866 866  
 FT ACT\_SITE 1026 1026  
 FT CARBOHYD 46 46  
 FT CARBOHYD 98 98  
 FT CARBOHYD 145 145  
 FT CARBOHYD 160 160  
 FT CARBOHYD 247 247  
 FT CARBOHYD 320 320  
 FT CARBOHYD 376 376  
 FT CARBOHYD 397 397  
 FT CARBOHYD 509 509  
 FT CARBOHYD 521 521  
 FT CARBOHYD 578 578  
 FT CARBOHYD 611 611  
 FT CARBOHYD 619 619  
 FT CARBOHYD 629 629  
 FT CARBOHYD 673 673  
 FT CARBOHYD 702 702  
 FT CARBOHYD 719 719  
 FT MOD\_RES 1057 1057  
 FT CONFLICT 25 25  
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 FT CONFLICT 783 784  
 FT CONFLICT 917 917  
 FT CONFLICT 1341 1367  
 FT  
 FT SEQUENCE 1367 AA; 152516 MW; EFC99704FIDCA266 CRC64;  
 Query Match 10.6%; Score 160.5; DB 1; Length 1367;  
 Best Local Similarity 24.8%; Pred. No. 1.7e-05;  
 Matches 53; Conservative 23; Mismatches 75; Indels 63; Gaps 6;  
 QY 44 QEAILACKTPKTKVSRLEWKKGRSVFVYQQTLOGDFKNRAEMIDFN----- 93  
 DB 562 QESVSLCTADPNTFENLTWYKLSQATSVHGESLTPVCXKNDALWKLNGTFPSNSTD 621  
 QY 94 ---IRKNVTRSDAGKYRC-----EVSAPSEQONLEEDTVTLEV 130  
 DB 622 ILIVAFQNASIQDQGVCSAQDKTKRKHCLVQLIILERMAMPITG-NLENQTFTI-- 678  
 QY 131 LVAFAVPSCEVPSSALSTVVELSCQDEKGNPAPEYTFWKGITLLENPLRGLSQSINSSY 190  
 DB 679 -----GETLEVTC-PASGNFTPHITWFKDNETLVSDSGIVURDGNRL 720  
 QY 191 TMTNKTGTLQNTVSKLDTGYSCEARNVGYRR 224  
 DB 721 TI-----RRVRKEDGGYLTQACNVLGAR 745  
 RESULT 12  
 NCW2\_MOUSE  
 ID NCW2\_MOUSE STANDARD; PRT; 837 AA.  
 AC O35136; O35962;  
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell  
 DE adhesion molecule) (R4B12).  
 DE NCAM2 OR OCAM OR RNCAM.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).  
 RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;  
 RX MEDLINE=97368238; PubMed=9221781;  
 RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,  
 RA Kagamiyama H., Mori K.;  
 RT "OCAM: A new member of the neural cell adhesion molecule family  
 RT related to zone-to-zone projection of olfactory and vomeronasal  
 RT axons".  
 RL J. Neurosci. 17:5830-5842(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;  
 RX MEDLINE=97476194; PubMed=9334170;  
 RA Alenius M., Bohm S.;  
 RT "Identification of a novel neural cell adhesion molecule-related gene  
 RT with a potential role in selective axonal projection".  
 RL J. Biol. Chem. 272:26083-26086(1997).  
 CC -!- FUNCTION: May play important roles in selective fasciculation and  
 CC zone-to-zone projection of the primary olfactory axons.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and  
 CC attached to the membrane by a GPI-anchor (short isoform).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoID=O35136-1; Sequences=Displayed;  
 CC Name=Short;  
 CC IsoID=O35136-2; Sequences=VSP\_002590;  
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and  
 CC vomeronasal neurons in a zone-specific manner.  
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
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 CC  
 CC EMBL; AF001287; AAB69125.1; -  
 CC EMBL; AF001286; AAB69124.1; -  
 CC EMBL; AF016619; AAC53375.1; -  
 CC MGD; MGI:97282; Ncam2.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00047; ig; 5.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00408; Igc2; 5.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 KW Cell adhesion; Transmembrane; Signal; GPI-anchor; Alternative splicing.  
 KW Immunoglobulin domain; Signal;  
 FT SIGNAL 1 19  
 FT CHAIN 20 837  
 FT DOMAIN 20 697  
 FT TRANSMEM 698 718  
 FT DOMAIN 719 837  
 FT DOMAIN 21 108  
 FT DOMAIN 113 202  
 FT DOMAIN 208 297





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DR InterPro: IPR002154; Neuregulin.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF02158; Neuregulin; 1.
DR SMART: SM00181; IGF; 1.
DR SMART: SM00408; IGF2; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
KW Transmembrane; Multigene family; Alternative splicing.
KW PROPEP 1 127
FT CHAIN 128 868 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
FT CHAIN 128 868 NEUREGULIN-2.
FT CHAIN 128 428 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 128 429 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT TRANSMEM 430 450 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 451 868 IG-LIKE C2-TYPE.
FT DOMAIN 253 348 SER/THR-RICH.
FT DOMAIN 346 356 EGF-LIKE.
FT DOMAIN 357 398 POLY-SER.
FT DOMAIN 22 32 POLY-SER.
FT DOMAIN 35 45 POLY-THR.
FT DOMAIN 56 59 POLY-ALA.
FT DOMAIN 103 106 POLY-PRO.
FT DOMAIN 739 745 POLY-PRO.
FT DISULFID 273 327 BY SIMILARITY.
FT DISULFID 361 375 BY SIMILARITY.
FT DISULFID 369 386 BY SIMILARITY.
FT DISULFID 388 397 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 108 Missing (in isoform 7).
FT VARSPLIC 220 222 PLV -> FFF (in isoform 3).
FT VARSPLIC 388 388 /FTID=VSP_003466.
FT VARSPLIC 389 868 /FTID=VSP_003467.
FT VARSPLIC 390 412 Missing (in isoform 5).
FT VARSPLIC 390 421 NGFGQRCLEKLPRLNPPPKQ -> VGYTGRCQCFAMV
FT VARSPLIC 390 421 /FTID=VSP_003469.
FT VARSPLIC 390 421 NGFGQRCLEKLPRLNPPPKQHLGFELKE -> VGYTG
FT VARSPLIC 414 421 /FTID=VSP_003470.
FT VARSPLIC 414 439 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 414 439 /FTID=VSP_003471.
FT VARSPLIC 440 868 HLGELKEAELEKRVLTITGICVA -> SVLWDTFGTGV
FT CONFLICT 117 117 S -> F (IN REF. 2).
FT CONFLICT 724 724 R -> H (IN REF. 2).
SQ SEQUENCE 868 AA; 93776 MW; 3C7D4D94DBB64DE2 CRC64;

Query Match
Best Local Similarity 27.7%; Score 157; DB 1; Length 868;
Matches 56; Conservative 24; Mismatches 86; Indels 36; Gaps 8;

QY 66 LGRSVFVYQTLQGB--FKVAREMDFNIRKNVTRSDAGKYRCEVSPSQGNLEE 123
DB 204 LERNQRVIFLEPEQPLVFETAPVDPN--GKNV--KKEVGKILCTDCATRPKLKKMS 260
QY 124 DTVTLEVLVAPVSCVPSPSALSGTVVELRCQDKGNPAPETWFKDGIIRLENPLRG 183
DB 261 QTGEV-----GEKQSLKCEAAAGNQPQSYRWFKDQKELNR-----S 296
QY 184 QSTNSSTMTNKTGTLQFNVSKLDTGEYCEARNVGVRCRCRGMQVDDLNI-----S 238

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DB 297 RDIRIKYNGRKNRSLQFNKVKVEDAGEYVCEAEINILGKDTVRG-RLHVSNSVTLLSSWS 355
QY 239 GIIAAVVVVVALVISVCGLGVCY 260
DB 356 GHARKCNETAKSYCVNG-GVCY 376

RESULT 14
NRG2_MOUSE
ID NRG2_MOUSE STANDARD; PRT; 756 AA.
AC P56974;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
DE (Divergent of neuregulin 1) (DON-1)].
GN NRG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97342638; PubMed=9168115;
RA Caraway K.L. III, Weber J.L., Unger M.J., Ledesma J., Yu N.,
RA Cassmann M., Lai C.;
RT "Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine
RT kinases";
RL Nature 387:512-516 (1997).
RN [2]
RP SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).
RX TISSUE=Choroid plexus;
RX MEDLINE=97342638; PubMed=9199335;
RA Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,
RA Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodearl A.D.J.,
RA Gearing D.P.;
RA "Characterization of a neuregulin-related gene, Don-1, that is highly
RT expressed in restricted regions of the cerebellum and hippocampus.";
RL Mol. Cell. Biol. 17:4007-4014 (1997).
CC -!- FUNCTION: Direct ligand for ERBB3 and ERBB4 tyrosine kinase
CC receptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors,
CC resulting in ligand-stimulated tyrosine phosphorylation and
CC activation of the ERBB receptors. May also promote the
CC heterodimerization with the EGF receptor.
CC -!- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=NRG2-16A;
CC IsoId=P56974-1; Sequence=Displayed;
CC Name=DON-1M;
CC IsoId=P56974-2; Sequence=VSP_003464;
CC Name=DON-1S; Synonyms=NRG2-5;
CC IsoId=P56974-3; Sequence=VSP_003462, VSP_003463;
CC Name=NRG2-10;
CC IsoId=P56974-4; Sequence=VSP_003460, VSP_003461;
CC -!- TISSUE SPECIFICITY: Highest expression in the brain, with lower
CC levels in the lung. In the cerebellum, found in granule and
CC Purkinje cells.
CC -!- DOMAIN: The cytoplasmic domain may be involved in the regulation
CC of trafficking and proteolytic processing. Regulation of the
CC proteolytic processing involves initial intracellular domain
CC dimerization (By similarity).
CC -!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
CC domain (By similarity).
CC -!- PTM: Proteolytic cleavage close to the plasma membrane on the
CC external face leads to the release of the soluble growth factor
CC form (By similarity).
CC -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By

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DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR00242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 7.  
DR Pfam; PF00047; ig; 3.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00700; FNTYPEPHPTASE.  
DR SMART; SM00060; FN3; 4.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
DR PROSITE; PS00556; TYR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
KW Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.  
FT SIGNAL 1 16  
FT CHAIN 17 1897  
FT DOMAIN 17 1250  
FT TRANSMEM 1251 1274  
FT DOMAIN 1275 1897  
FT DOMAIN 23 113  
FT DOMAIN 125 214  
FT DOMAIN 222 304  
FT DOMAIN 1360 1606  
FT DOMAIN 1649 1897  
FT ACT\_SITE 1538 1538  
FT ACT\_SITE 1829 1829  
FT CARBOHYD 107 107  
FT CARBOHYD 240 240  
FT CARBOHYD 285 285  
FT CARBOHYD 711 711  
FT CARBOHYD 956 956  
FT MUTAGEN 1538 1538  
SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;  
Query Match 10.3%; Score 156; DB 1; Length 1897;  
Best Local Similarity 25.8%; Pred.No. 6e-05;  
Matches 59; Conservative 35; Mismatches 89; Indels 46; Gaps 10;  
QY 11 LLLLYLVVALGYHKAYGFSAPKQQVVTAVYQCEAILACKT---PKTKVKSRLWKKLK 67  
DB 8 LVMLGLVAGAGHDSKVPFIKVPEDQ---TGLSGGVASFVCOATCEPK----PRITWKKG 60  
QY 68 RSVSFVYYQQTLOGDFKNRAEMIDFN-----IRKNV-TRSDAGKYRCEVSAPSEQQN 120  
DB 61 KKVS-----SQRFVIEFDGAGSVLRIQPLRVQRDEAIVECTATNSLGEINT 108  
QY 121 LEEDTVTLVLVAVPSC-----VPSSALSGTVVELRCODKEGNAPETWFKDGIR 174  
DB 109 SAKLSVLEEELPPGFPIDGPGPOLKVVERKARTATML---CA-AGGNPDPEISWFKDPLP 164  
QY 175 LLENPRLGQSNTSNYSYTMNTKTGTLQNTVSKLDTGYSCEARNSVGVR 223  
DB 165 V-----DPATSNGRIRQLRSGALQIESSEESDQGYECVATNSAGTR 206

Search completed: July 15, 2004, 23:53:11  
Job time : 13.7487 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:33 ; Search time 52.5882 Seconds

(without alignments)  
1787.936 Million cell updates/sec

Title: US-09-852-797-76

Perfect score: 1521

Sequence: 1 MARRSRRLRLRLRLVLA.....SSKATTMSNDLFHGTSPFII 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:\*\*

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioplasmid:\*  
17: sp\_archaeplastid:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1215	79.9	298	11 Q9JI59	Q9JI59 mus musculus
2	1212	79.7	298	11 Q8CE95	Q8CE95 mus musculus
3	1212	79.7	298	11 Q8C5K9	Q8C5K9 mus musculus
4	507.5	33.4	181	11 Q9CWD9	Q9CWD9 mus musculus
5	499	32.8	310	11 Q9D8B7	Q9D8B7 mus musculus
6	499	32.8	310	11 Q9EPK4	Q9EPK4 mus musculus
7	495	32.6	310	11 Q9D1M9	Q9D1M9 mus musculus
8	481	31.6	310	4 Q9BX67	Q9BX67 homo sapien
9	481	31.6	355	4 Q8WML8	Q8WML8 homo sapien
10	480	31.6	309	4 Q96FL1	Q96FL1 homo sapien
11	453	29.8	300	13 Q7SYQ7	Q7SYQ7 xenopus lae
12	435	28.6	289	13 Q7ZWT0	Q7ZWT0 xenopus lae
13	421	27.7	300	11 Q8VC39	Q8VC39 mus musculus
14	409.5	26.9	300	11 Q9JHY1	Q9JHY1 rattus norv
15	393.5	25.9	299	4 Q9YB22	Q9YB22 homo sapien
16	315.5	20.7	173	11 Q9JKD5	Q9JKD5 rattus norv

#### ALIGNMENTS

RESULT 1

Q9JI59 PRELIMINARY; PRT; 298 AA.

AC Q9JI59; DT 01-OCT-2000 (TREMELrel. 15, Created)  
 AC Q9JI59; DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Vascular endothelial junction-associated molecule (Junctional adhesion molecule-3) (2410030G213ik protein).  
 GN JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=20317114; PubMed=10779521;  
 RA Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;  
 RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of the Immunoglobulin Superfamily, Is Localized to Intercellular Boundaries of Endothelial Cells."  
 RT J. Biol. Chem. 275:19139-19145(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX PubMed=11036763;  
 RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;  
 RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular Family?"  
 RT Curr. Top. Microbiol. Immunol. 251:91-98(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;  
 RX MEDLINE=21085560; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saio T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito K.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Q91664 xenopus lae  
 Q9PWR4 gallus gall  
 Q9YGH1 gallus gall  
 Q922D5 mus musculus  
 Q9JKA5 mus musculus  
 Q9YGV5 gallus gall  
 Q91665 xenopus lae  
 Q7Z2Q1 homo sapien  
 Q8XK7 homo sapien  
 Q9TU80 canis faml  
 Q96T50 homo sapien  
 Q96AP7 homo sapien  
 Q8WV3 bos taurus  
 Q925F2 mus musculus  
 Q9D2J4 mus musculus  
 Q9XKV4 homo sapien  
 Q95KI3 macaca fasc  
 Q90Y50 brachydanio  
 Q9TU79 sus scrofa  
 Q8N4F1 homo sapien  
 Q8IRS5 drosophila  
 Q9DA22 mus musculus  
 Q9D9J0 mus musculus  
 Q91W66 mus musculus  
 Q9DBJ8 mus musculus  
 Q9CVA4 mus musculus  
 Q8ND2 homo sapien  
 Q9NX42 homo sapien



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Best Local Similarity 78.6%; Pred. No. 1.8e-105;
Matches 235; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

QY 1 MARRSRHELLLLRLVYLVALGVHKGAFSPKXQ-QQVTVAVYQAEALACKTPKKTYS 59
Db 1 MARSQGLMLLLHLHYLVLDYHKGAFSADKHQEVTVIEFQAILACKTPKKTTS 60

QY 60 RLEWKKLGRSVSFYVYQQTQQGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQ 119
Db 61 RLEWKKVQGVSLVYVYQQALQGGDFKRAEMIDFNIRIKNVTSDAGEYRCEVSAPTEQQ 120

QY 120 NLEEDTVTLVLEVL 131
Db 121 NLQEDKVMLEVL 132

QY 180 RLSQSQTNSSTYMTNTKGTGLQFNVTSKLDTGEYSCSEARNVSVYRRCPGKRMQVDDNLISG 239
Db 181 K-GRTHNNSSTYMTNTKSGILQFNWISQDSEYVCEARNVSVGRRCPGKRMQVDDNLISG 239

QY 240 IIAVVVVVALVIVCGLGVCYAKRGYFSKTSFQKNSSSKATTSNDFKHTKFI 298
Db 240 IIAVVVVVAFVIVCGLGTCYAKRGYFSKTSFQKNSKATTSNDFKHTKFI 298

RESULT 4
Q9CWD9 PRELIMINARY; PRT; 181 AA.
AC Q9CWD9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2410167M24Rik protein (Junction cell adhesion molecule 2).
GN JAM2 OR JCAM2 OR 2410167M24Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK010826; BAB27208.1; -.
DR ENBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 181 AA; 20330 MW; 603B6114FBB11AEB CRC64;

Query Match 33.4%; Score 507.5; DB 11; Length 181;
Best Local Similarity 76.5%; Pred. No. 1.5e-39;
Matches 101; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 MARRSRHELLLLRLVYLVALGVHKGAFSPKXQ-QQVTVAVYQAEALACKTPKKTYS 59
Db 1 MARSQGLMLLLHLHYLVLDYHKGAFSADKHQEVTVIEFQAILACKTPKKTTS 60

QY 60 RLEWKKLGRSVSFYVYQQTQQGDFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQ 119
Db 61 RLEWKKVQGVSLVYVYQQALQGGDFKRAEMIDFNIRIKNVTSDAGEYRCEVSAPTEQQ 120

QY 120 NLEEDTVTLVLEVL 131
Db 121 NLQEDKVMLEVL 132

RESULT 5
Q9DBB7 PRELIMINARY; PRT; 310 AA.
AC Q9DBB7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK010826; BAB27208.1; -.
DR ENBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu X., Nikaide I., Pasole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Poffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboidi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003326; BAB22715.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34819 MW; 5692BCAD68EA81D CRC64;

Query Match 32.6%; Score 496; DB 11; Length 310;
Best Local Similarity 37.0%; Pred. No. 3.7e-38;
Matches 117; Conservative 61; Mismatches 112; Indels 26; Gaps 9;

QY 1 MARRSRHRL-----LILLRLVLYVALGYHKAYGFSAPKDDQVVTVXVYQEAAILAC-K 51
DB 3 LSRRRLRLVRLPDPFLLLFRGCM-----FVNLKSNRPVPH--EFESVELSCII 55

QY 52 TPKTKTVXSRLEWKKL-GRSVFYVYQTLQGDFFKNRAEMI-DNIRIKNVTNRSDAGKYRC 109
DB 56 TDSQTSDPRIEWKKIQDEQTYVFFDNKIQDGLAGRAEILGKTSLKINWVTRSDSALY 115

QY 110 EVSAPSEQQNLEEDVTLEVLVAPVAPVSPCEVPSSALSGLTVVLRCDKEGNPAPETV 169
DB 116 EVVALNDR-KEVDEIVIELTVQVKPVTFCRVPRAVPGVGMKATLHQCSESGHPRPHYS 174

QY 170 KDGRILLENPRLGQSNTSSYTNMTKTGTLQFNTVSKLDTGEYSCEARNVSVYRCPGKR 229
DB 175 RNDVPLPTDSRANPRFNSSFLNSETGLVFTAVHKDDSGQYVCIASNDAGARCEGD 234

QY 230 MQVDDNLNIGIIAAVVVVALVIVSGVLGVCYAKRGYF--SKE-----TSFQKSNSSKA 282
DB 235 MEVVDNLNIGIIGVLVLLVLAIVTMGICAYRRGCFISSKQDGSYKSPGRHGVNYI 294

QY 283 TTMSNDFKHTKSFII 298
DB 295 RTSEEGDFKHIAFVI 310

RESULT 8
Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion
DE molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein
DE FLJ90288) (Hypothetical protein FLJ90288).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_taxid=9606;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

```

```

RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Aurand-Lions M.A., Johnson-leger C., Wong C., Dupasquier L.;
RA Aurand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RA "Characterization of Junctional Adhesion Molecule-3 on Human
RT Platelets: A New Member of Immunoglobulin Superfamily.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RP Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AAK27221.1; -.
DR EMBL; AJ344431; CAC69845.1; -.
DR EMBL; AF448478; AAM20925.1; -.
DR EMBL; AK074769; BAC11195.1; -.
DR EMBL; AK075309; BAC11538.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30 POTENTIAL.
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EADAB9 CRC64;

Query Match 31.6%; Score 481; DB 4; Length 310;
Best Local Similarity 35.8%; Pred. No. 9.6e-37;
Matches 114; Conservative 60; Mismatches 116; Indels 28; Gaps 10;

QY 1 MARRSRHRL-----LILLRLVLYVALGYHKAYGFSAPKDDQVVTVXVYQEAAILAC 50
DB 1 MARRSRHRLCARLPDPFLLLFRCLIG-----FVNLKSNRPVPH--EFESVELSC 53

QY 51 -KTPKTKTVXSRLEWKKL-GRSVFYVYQTLQGDFFKNRAEMI-DNIRIKNVTNRSDAGKY 107
DB 54 IITDSQTSDPRIEWKKIQDEQTYVFFDNKIQDGLAGRAEILGKTSLKINWVTRSDSALY 113

QY 108 RCEVSAPSEQQNLEEDVTLEVLVAPVAPVSPCEVPSSALSGLTVVLRCDKEGNPAPETV 167
DB 114 RCEVARNDR-KEIDEIVIELTVQVKPVTFCRVPRAVPGVGMKATLHQCSESGHPRPHYS 172

QY 168 WFKDGIRILENPRLGQSNTSSYTNMTKTGTLQFNTVSKLDTGEYSCEARNVSVYRCPG 227
DB 173 WYNDVPLPTDSRANPRFNSSFLNSETGLVFTAVHKDDSGQYVCIASNDAGARCEB 232

QY 228 KMQVDDNLNIGIIAAVVVVALVIVSGVLGVCYAKRGYF--SKE--TSFQ---KSNSSS 280
DB 233 QEMEVVDNLNIGIIGVLVLLVLAIVTMGICAYRRGCFISSKQDGSYKSPGRHGVNYI 292

QY 281 KATTMSNDFKHTKSFII 298
DB 293 YIRTDEEGDFKHKSFFVI 310

RESULT 9

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[illegible]

```
QY 4 RSRHLLLLLYLVVALGYHAYGSAFKDQVQVTAIXYQEAAILACKTPKTKVXSLEW 63
DB 6 KAGRKLFLFTSMILGSLVQKGSVYTAQSDVQVPE-----NESIKLJCTYSGFSSPRVW 61
QY 64 KKL-GRSVFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSQOGNLE 122
DB 62 KFOQSITLVCYNSQITAPADRVTFSSSGITFSSVTRKDNGETCWVS--EEGGQNYG 119
QY 123 EDTVLVLVAVPAPSCVPSALSCTVVELRCDQKGNPAPEYTWKDGIRLLENPLRG 182
DB 120 EVSIHLTVLVPSPKPTTISVPSVTIGNRAVLTCSEHDGSPPEYSWFKDGISMLTADAKK 179
QY 183 SOS-TNSSYTNMTKTGTQFNTVSKLDTGEYSCEARNVSVG-YRCPGKRQVDDLNISGI 240
DB 180 TRAFNNSFTIDPKSGDLIFPVTAFDGSEYVCOQNGYGTAMRSEAAHMDAVELNVGGI 239
QY 241 IAAVVVALVTSVCGLVGCYQAQRKGYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 297
DB 240 VAAVLVTLILGLLIFGVWFAYSRGYFERTKKGTAQPKKVIYQSPSTRSEGEFKQTSSFL 299
QY 298 I 298
DB 300 V 300

RESULT 14
Q9JHV1 PRELIMINARY; PRT; 300 AA.
AC Q9JHV1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Junctional adhesion molecule JAM.
GN JAM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley;
RA Mashima H., Kojima I.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276998; AAF78250.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;

Query Match 26.9%; Score 409.5; DB 11; Length 300;
Best Local Similarity 34.3%; Pred. No. 4.8e-30;
Matches 95; Conservative 49; Mismatches 98; Indels 35; Gaps 6;

QY 28 GFSAKPDQVQVTAIXYQEAAILACKTPKTKVXSLEWKL-GRSVFVYQOTLQDGFKNR 86
DB 53 GFSP-----RVEWKFVQGSTALVCYNNQITVPIADR 85
QY 87 AEMIDFNIRIKNVTSDAGKYRCEVSAPSQOGNLEEDTVTLVLVAVPAPSCVPSALS 146
DB 86 VTFSSSGITFSSVTRKDNGETCWVS--EDGGQNYGEVSIHLTVLVPSPKPTVSISSVT 143
QY 147 SGTVELRCODKGNPAPEYTWKDGIRLLENPLRGQS--TNSSYTNMTKTGTQFNTVS 205
DB 144 IGRNAVLTCSHDGSPPEYSWFKDGVPMLTADAKKTRAFINSYTIIDPKSGDLVFDVPS 203
QY 206 KLDTGEYSCEARNVSVG-YRCPGKRQVDDLNISGIIAAVVVVALVTSVCGLVGCYQAQRK 264
DB 204 AFDSGEYVCAQNGYGTAMRSEAVRMEAVELNVGGIVAALVTLILGLLIFGVWFAYSR 263
QY 265 GYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 298
DB 265 GYF---SKETSFOKSNSSSKATTMSNDPKHTKXFI 298
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```
DB 264 GYFERTKGTAPKGVYQSPARSSEGEFKQTSSFLV 300

RESULT 15
Q9Y5B2 PRELIMINARY; PRT; 259 AA.
AC Q9Y5B2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA Foley C., Parkos C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 1.
OX Immunoglobulin domain.
KW
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911562D0 CRC64;

Query Match 25.9%; Score 393.5; DB 4; Length 259;
Best Local Similarity 36.9%; Pred. No. 1.2e-28;
Matches 87; Conservative 41; Mismatches 97; Indels 11; Gaps 4;

QY 59 SVSFVYQOTLQDGFKNRAEMIDFNIRIKNVTSDAGKYRCEVSAPSQOGNLEEDTVTL 128
DB 29 SCAYSGFSPPRAASYEDRVTFLTGITPKSVTRBDTGTTCMTF--EEGGNSYGEVKVKL 86
QY 129 EVLVAPAPSCVPSALSCTVVELRCODKGNPAPEYTWKDGIRLLENPLRGQSQTNS 188
DB 87 IVLVPPSKPTVNIPISSAIGNRAVLTCSEQDGSPPSEYTWKDGIVMPTNPKSTRAFNS 146
QY 189 SYTNMTKTGTQFNTVSKLDTGEYSCEARNVSVYRRCPGK-RMQVDDLNISGIIAAVVVV 247
DB 147 SYVLNPTTGELVDFDPLSASDTGEYSCEARNGYTGMTSNVAVRMEAVERNVGVIAAALVT 206
QY 248 ALVISVCGLVGCYQAQRKGYFSKETSFOKSNSSSKA-----TTMSNDPKHTKXFI 298
DB 207 LLLGLVFGVWFAYSRGHFDRP---KKGTSKKVIYQSPARSSEGEFKQTSSFLV 259

Search completed: July 15, 2004, 23:54:29
Job time : 54.5882 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 23:48:38 ; Search time 19.7112 Seconds  
(without alignments)  
1089.410 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388

Sequence: 1 YKAYGFSAPKQQVTVAV.....LQDFFKRAEMIDFNIRIKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1990s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	99.2	235	6 AAO30179	Human nov
2	385	99.2	298	2 AAW85457	Secreted
3	385	99.2	298	4 AAU00512	Human jun
4	385	99.2	298	5 ABP61801	Human pol
5	385	99.2	298	6 ABR58532	Human vas
6	385	99.2	298	6 AAO16452	Human jun
7	385	99.2	303	4 AAM23693	Human EST
8	385	99.2	312	2 AAY23324	A33 relat
9	385	99.2	312	2 AAY08060	Human PRO
10	385	99.2	312	2 AAY13354	Amino aci
11	385	99.2	312	3 AAB33421	Human PRO
12	385	99.2	312	3 AAY70668	Human PRO
13	385	99.2	312	3 AAB24401	Human PRO
14	385	99.2	312	3 ADC78384	Human PRO
15	385	99.2	312	4 AAB80222	Human PRO
16	385	99.2	312	4 AAU00821	Human imm
17	385	99.2	312	4 AAU12339	Human PRO
18	385	99.2	312	4 AAB53081	Human ang
19	385	99.2	312	6 ABU71600	Human PRO
20	385	99.2	312	6 ABO17783	Novel hum
21	385	99.2	312	6 ABU71455	Human PRO
22	385	99.2	312	6 ABU81037	Human PRO
23	385	99.2	312	6 ABU71901	Human sec
24	385	99.2	312	6 ABO01784	Novel hum
25	385	99.2	312	6 ABU66737	Human PRO

#### ALIGNMENTS

##### RESULT 1

AAO30179  
ID AAO30179 standard; protein; 235 AA.

XX AC AAO30179;

XX DT 03-SEP-2003 (first entry)

XX DE Human novel splice variant of VEJAM (NOJAM).

XX KW Human; forensic analysis; chromosome marker; organelle-specific marker;  
XX KW novel-related disorder; neurological disorder; gene therapy; nootropic;  
XX KW neuroprotective; vascular endothelial junctional adhesion molecule;  
XX KW VEJAM; NOJAM.

XX OS Homo sapiens.  
XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..28  
XX FT /label= Signal\_peptide  
XX FT Protein 29..235  
XX FT /note= "Human mature NOJAM protein"

XX WO2003046180-A2.

XX PD 05-JUN-2003.

XX PF 25-NOV-2002; 2002WO-EP013210.

XX PR 28-NOV-2001; 2001US-0334147P.

XX PR 14-DEC-2001; 2001US-0340463P.

XX PR 18-APR-2002; 2002US-0373947P.

XX PA (GEST ) GENSET SA.

XX PI Bejanin S, Tanaka H;

XX XX WPI; 2003-505202/47.

XX DR N-PSDB; AAL60897.

XX XX

XX PT New isolated polynucleotides and polypeptides useful as reagents in  
XX PT forensic analyses, as chromosome markers, as tissue/cell/organelle-  
XX PT specific markers, in producing expression vectors, or in screening and  
XX PT diagnostic assays.

XX PS Claim 2; Page 229; 242pp; English.

XX XX

CC The invention relates to human novel polynucleotide and polypeptide  
CC sequences useful as reagents in forensic analyses, as chromosome markers,  
CC as tissue/cell/organelle-specific markers, in producing expression  
CC vectors, or in screening and diagnostic assays. The invention is used as  
CC reagents in screening and diagnostic assays for abnormal novel expression  
CC and/or biological activity, and in screening compounds that may be used  
CC in the treatment of novel-related disorders, e.g. neurological disorders.  
CC The novel gene is also used in gene therapy. The present sequence is  
CC human novel splice variant of vascular endothelial junctional adhesion  
CC molecule (VEJAM), NOJAM of the invention  
XX  
XX Sequence 235 AA;  
SQ

Query Match 99.2%; Score 385; DB 6; Length 235;  
Best Local Similarity 97.4%; Pred. No. 3.9e-45;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTA VYQEA I LACKTPKKT VXSRLWK KLGSRVSFVYYQQT LQGD 60  
DB 23 YHKAYGFSAPKDDQVVTA VYQEA I LACKTPKKT VXSRLWK KLGSRVSFVYYQQT LQGD 82  
QY 61 FKQRAEMIDFNIRIKN 76  
DB 83 FKQRAEMIDFNIRIKN 98

RESULT 2  
AAW85457  
ID AAW85457 standard; protein; 298 AA.  
XX  
AC AAW85457;  
XX  
DT 25-FEB-1999 (first entry)  
XX  
DE Secreted protein encoded by clone ct864\_4.  
XX  
KW Secreted protein; nutritional activity; immune stimulating; vaccine;  
KW suppressing activity; haematopoiesis regulating activity;  
KW tissue growth activity; activin; inhibin activity; chemotaxis;  
KW chemokinetic activity; haemostasis; thrombolytic activity; receptor;  
KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;  
KW tumour inhibition; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO9842739-A2.  
XX  
PD 01-OCT-1998.  
XX  
PF 20-MAR-1998; 98WO-US005653.  
XX  
PR 21-MAR-1997; 97US-00822167.  
PR 19-MAR-1998; 98US-00044466.  
XX  
PA (GEMY) GENETICS INST INC.  
XX  
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
PI Spaulding V, Agostino MJ;  
XX  
DR WPI; 1998-609890/51.  
DR N-PSDB; AAW82780.  
XX

XX New polynucleotides encoding secreted human proteins - derived from human  
PT foetal brain, adult brain, foetal kidney, placenta or adult pineal gland  
PT cDNA libraries.  
XX  
PS Claim 17; Page 73-74; 113pp; English.  
XX

XX The present sequence represents a secreted protein. The polynucleotide  
CC and secreted protein are predicted to have biological activities which  
CC would make them suitable for treating, preventing or ameliorating medical  
CC conditions in humans and animals, although no supporting data is given.  
CC Suggested activities include nutritional activity, immune stimulating  
CC

CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating  
CC activity, tissue growth activity, activin/inhibin activity,  
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,  
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour  
CC invasion suppressor activity, and tumour inhibition activity (no data is  
CC given in the specification to support these activities). The  
CC polynucleotide is also stated to be useful for gene therapy  
XX  
XX Sequence 298 AA;  
SQ

Query Match 99.2%; Score 385; DB 2; Length 298;  
Best Local Similarity 97.4%; Pred. No. 5.2e-45;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTA VYQEA I LACKTPKKT VXSRLWK KLGSRVSFVYYQQT LQGD 60  
DB 23 YHKAYGFSAPKDDQVVTA VYQEA I LACKTPKKT VXSRLWK KLGSRVSFVYYQQT LQGD 82  
QY 61 FKQRAEMIDFNIRIKN 76  
DB 83 FKQRAEMIDFNIRIKN 98

RESULT 3  
AAU00512  
ID AAU00512 standard; protein; 298 AA.  
XX  
AC AAU00512;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Human junctional adhesion protein (JAM2).  
XX

XX Junctional adhesion protein; JAM2; cellular localisation;  
KW cellular expression; immunoprecipitation; stroke; phosphorylation;  
KW glycosylation; paracellular migration; inflammatory disease; arthritis;  
KW asthma; rheumatoid arthritis; inflammatory bowel disease;  
KW Crohn's disease.  
XX  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FH Peptide 1..28 /note= "Possible signal peptide #2"  
FT Peptide 1..20 /note= "Possible signal peptide #1"  
FT Protein 21..298 /note= "Possible mature JAM2 #1"  
FT Protein 29..298 /note= "Possible mature JAM2 #2"  
FT Domain 237..254 /note= "Transmembrane domain"  
XX  
PN WO200114404-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 23-AUG-2000; 2000WO-US023158.  
XX  
PR 24-AUG-1999; 99US-0150459P.  
XX  
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
XX

XX Cunningham S, Trindad Arrate Barros M;  
PI N-PSDB; AAS00512.  
XX  
DR WPI; 2001-218425/22.  
XX

XX Novel nucleic acids encoding human junctional adhesion protein useful for  
PT producing antibodies that are suitable for therapeutic purposes.  
XX  
PS Claim 4; Page 46-47; 51pp; English.  
XX

CC The sequence represents a human junctional adhesion molecule 2 (JAM2).  
CC The polynucleotide encoding the polypeptide is useful for recombinant  
CC production of JAM-2 protein, which in turn is useful for the production  
CC of antibodies. The antibodies may be used for probing cellular  
CC localisation and/or expression of JAM2 in tissues under normal and  
CC disease states, for immunoprecipitating JAM2 protein from cells and/or  
CC stroke tissues to determine whether it is modified by glycosylation and  
CC phosphorylation, and for determining JAM2 function. The antibodies  
CC inhibit interaction of JAM2 with inflammatory cells or influence their  
CC paracellular migration, and is therefore useful for alleviating  
CC inflammatory diseases such as arthritis, asthma, rheumatoid arthritis,  
CC inflammatory bowel disease and Crohn's disease  
XX  
SQ Sequence 298 AA;  
Query Match 99.2%; Score 385; DB 4; Length 298;  
Best Local Similarity 97.4%; Pred. No. 5.2e-45;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 60  
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVSSRLEWKKLGRSVSFYVYQQTLOGD 82  
QY 61 FKNRAEMIDFNIRIKN 76  
DB 83 FKNRAEMIDFNIRIKN 98  
RESULT 4  
ABP61801 standard; protein; 298 AA.  
XX AC ABP61801;  
XX DT 04-OCT-2002 (first entry)  
XX DE Human polypeptide SEQ ID NO 155.  
XX KW Human; cytostatic; antirheumatic; antiarthritic; vulnary; analgesic;  
KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;  
KW neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;  
KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;  
KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;  
KW cytokine; cell proliferation; cell differentiation; autoimmune disease;  
KW stem cell; growth factor; nervous system disease; neuropathy;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
KW osteoporosis; severe combined immunodeficiency; SCID; infection;  
KW multiple sclerosis; rheumatoid arthritis; gene therapy.  
XX OS Homo sapiens.  
XX PN US2002065394-A1.  
XX PD 30-MAY-2002.  
XX PF 22-DEC-2000; 2000US-00745763.  
XX PR 18-MAR-1998; 98US-00040963.  
XX PA (JACO/) JACOBS K.  
XX PA (MCCO/) MCCOY J M.  
XX PA (LAVA/) LAVALLIE E R.  
XX PA (COLL/) COLLINS-RACIE L A.  
XX PA (EVAN/) EVANS C.  
XX PA (NERB/) MERBERG D.  
XX PA (TREA/) TREACY M.  
XX PA (SPAU/) SPAULDING V.  
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
XX Merberg D, Treacy M, Spaulding V;  
XX WPI: 2002-582343/62.  
XX N-PSDB; ABQ92017.

XX Novel secreted or transmembrane protein and polynucleotide encoding the  
PT protein, useful for diagnosis and treatment of neurological disorders,  
XX cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.  
PS Claim 54; Page 116-117; 284pp; English.  
XX The invention relates to human secreted or transmembrane protein (I),  
CC their fragments and is encoded by specific complementary deoxyribonucleic  
CC acid (cDNA) inserts (II), where the protein is substantially free from  
CC other mammalian proteins. (I) are useful for preventing, treating or  
CC ameliorating a medical condition, especially immunological treatment or  
CC prevention of tumours. (I) exhibits activity relating to angiogenesis,  
CC cytokine, cell proliferation, cell differentiation, antiinflammatory,  
CC stem cell growth factor activity and activin or inhibin-related  
CC activities. (I) can be used to manipulate stem cells in culture to give  
CC rise to neuroepithelial cells that can be used to augment or replace  
CC cells damaged by illness, autoimmune disease, accidental damage or  
CC genetic disorders. (I) induces the proliferation of neural cells and  
CC regeneration of nerve and brain tissue and is useful for the treatment of  
CC central and peripheral nervous system diseases and neuropathies, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic  
CC activity, regulation of haematopoiesis and is useful for treating myeloid  
CC or lymphoid cell disorders, platelet disorders such as thrombocytopaenia  
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,  
CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or  
CC periodontal disease. (I) is also useful for gut protection or  
CC regeneration and treatment of lung or liver fibrosis, reperfusion injury  
CC in various tissues, various immune deficiencies and disorders including  
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,  
CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,  
CC such as asthma or other respiratory problems. (II) is useful to express  
CC recombinant protein, as markers for tissues in which the corresponding  
CC protein is preferentially expressed and in gene therapy. The present  
CC sequence is that of a polypeptide of the invention  
SQ Sequence 298 AA;  
Query Match 99.2%; Score 385; DB 5; Length 298;  
Best Local Similarity 97.4%; Pred. No. 5.2e-45;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVXSRLEWKKLGRSVSFYVYQQTLOGD 60  
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTKVSSRLEWKKLGRSVSFYVYQQTLOGD 82  
QY 61 FKNRAEMIDFNIRIKN 76  
DB 83 FKNRAEMIDFNIRIKN 98  
RESULT 5  
ABR58532 standard; protein; 298 AA.  
XX AC ABR58532;  
XX DT 09-JUL-2003 (first entry)  
XX DE Human vascular endothelial junction-associated molecule protein.  
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
KW heart disease; atherosclerosis; endometriosis.  
XX OS Homo sapiens.  
XX PN WO2003025138-A2.  
XX PD 27-MAR-2003.  
XX





OS Homo sapiens.  
 XX WO200154477-A2.  
 XX PD 02-AUG-2001.  
 XX PF 25-JAN-2001; 2001WO-US002687.  
 XX PR 25-JAN-2000; 2000US-00491404.  
 XX PR 17-JUL-2000; 2000US-00617746.  
 XX PR 03-AUG-2000; 2000US-00631451.  
 XX PR 15-SEP-2000; 2000US-00663870.  
 XX PA (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V,  
 XX Cao Y, Dmanac RA, Zhang J, Werhman T;  
 XX WPI; 2001-476164/51.  
 XX N-PSDB; AAH98352.  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 XX antibodies and research use.  
 XX Claim 20; Page 878-879; 1275pp; English.  
 XX The present invention provides the protein and coding sequences of novel  
 XX proteins from a variety of organisms, including human, dog, cat, horse,  
 XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 XX urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 XX from the organism of interest. They can be used in diagnostics,  
 XX forensics, gene mapping, identification of mutations, to assess  
 XX biodiversity and for nutritional purposes. The present sequence is a  
 XX protein of the invention  
 XX Sequence 303 AA;  
 XX  
 XX Query Match 99.2%; Score 385; DB 4; Length 303;  
 XX Best Local Similarity 97.4%; Pred. No. 5.3e-45;  
 XX Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YHKAYGFSAPKQQQVTVAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 60  
 Db 23 YHKAYGFSAPKQQQVTVAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 82  
 QY 61 FKNRAEMIDFNIRIKN 76  
 Db 83 FKNRAEMIDFNIRIKN 98  
 RESULT 8  
 AAY23324  
 ID AAY23324 standard; protein; 312 AA.  
 XX AC AAY23324;  
 XX DT 02-SEP-1999 (first entry)  
 XX DE A33 related antigen PRO245.  
 XX DE A33 related antigen; PRO301; PRO362; PRO245; inflammatory disease;  
 XX tumour.  
 XX Homo sapiens.  
 XX WO9927098-A2.  
 XX PD 03-JUN-1999.  
 XX XX 20-NOV-1998; 98WO-US024855.  
 XX XX 21-NOV-1997; 97US-0066364P.  
 XX PR 20-MAR-1998; 98US-0078936P.

PR 17-SEP-1998; 98WO-US019437.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi A, Fong S, Goddard A, Gurney AL, Napier MA, Tumas D;  
 XX Wood WI;  
 XX WPI; 1999-404743/34.  
 XX DR N-PSDB; AAX81770.  
 XX Antigen PRO301, PRO362 and PRO245 related to A33.  
 XX Example 3; Fig 11; 122pp; English.  
 XX The specification describes A33 related antigens PRO301, PRO362 and  
 XX PRO245. The methods and compositions of the invention are useful for the  
 XX treatment and diagnosis of inflammatory disease and tumours in mammals.  
 XX Such inflammatory diseases include of inflammatory bowel disease,  
 XX systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic  
 XX arthritis, spondyloarthropathies, systemic sclerosis, scleroderma,  
 XX idiopathic inflammatory myopathies, dermatomyositis, polymyositis,  
 XX Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic  
 XX anemia, immune pancytopenia, paroxysmal nocturnal hemoglobinuria,  
 XX autoimmune thrombocytopenia, idiopathic thrombocytopenic purpura, immune-  
 XX mediated thrombocytopenia, thyroiditis, Grave's disease, Hashimoto's  
 XX thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis,  
 XX diabetes mellitus, immune-mediated renal disease, glomerulonephritis,  
 XX tubulointerstitial nephritis, demyelinating diseases of the central and  
 XX peripheral nervous systems such as multiple sclerosis, idiopathic  
 XX polyneuropathy, hepatobiliary diseases, infectious hepatitis A, B, C, D,  
 XX E, nonhepatotropic viruses, autoimmune chronic active hepatitis, primary  
 XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 XX inflammatory and fibrotic lung diseases, gluten-sensitive enteropathy,  
 XX Whipple's disease, autoimmune or immune-mediated skin diseases allergic  
 XX diseases of the lung such as eosinophilic pneumonias, idiopathic  
 XX pulmonary fibrosis and hypersensitivity pneumonitis transplantation  
 XX associated diseases disease. The present sequence represents PRO245  
 XX Sequence 312 AA;  
 XX  
 XX Query Match 99.2%; Score 385; DB 2; Length 312;  
 XX Best Local Similarity 97.4%; Pred. No. 5.5e-45;  
 XX Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YHKAYGFSAPKQQQVTVAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 60  
 Db 23 YHKAYGFSAPKQQQVTVAVYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGD 82  
 QY 61 FKNRAEMIDFNIRIKN 76  
 Db 83 FKNRAEMIDFNIRIKN 98  
 RESULT 9  
 AAY08060  
 ID AAY08060 standard; protein; 312 AA.  
 XX AC AAY08060;  
 XX DT 11-SEP-2000 (first entry)  
 XX DE Human PRO245 protein.  
 XX Inflammatory cell infiltration; immune response; T cell proliferation;  
 XX anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;  
 XX T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;  
 XX inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;  
 XX diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;  
 XX multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;  
 XX sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;  
 XX skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;  
 XX food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;  
 XX idiopathic pulmonary fibrosis; graft rejection; PRO245; human.

XX OS Homo sapiens.  
 XX EN WO9914241-A2.  
 XX PD 25-MAR-1999.  
 XX PF 17-SEP-1998; 98WO-US019437.  
 XX PR 17-SEP-1997; 97US-00591119P.  
 XX PR 18-SEP-1997; 97US-0059263P.  
 XX PR 28-OCT-1997; 97US-00633550P.  
 XX PR 12-NOV-1997; 97US-0065186P.  
 XX PR 21-NOV-1997; 97US-00663364P.  
 XX PR 24-NOV-1997; 97US-0066770P.  
 XX PR 04-JUN-1998; 98US-0088026P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;  
 XX DR WPI; 1999-229499/19.  
 XX DR N-PSDB; AAX37664.  
 XX PT Composition containing novel polypeptide PRO245, its agonist or  
 XX PT antagonist.  
 XX PS Example 1; Fig 2; 177pp; English.  
 XX CC This invention describes a novel composition containing (apart from a  
 CC carrier or excipient), a novel PRO245 polypeptide (I), its agonist or  
 CC antagonist, or their fragments, for modulating: (i) infiltration of  
 CC inflammatory cells into tissue; (ii) an immune response; or (iii) T cell  
 CC proliferation. The composition increases or decreases any of the effects  
 CC (i)-(iii). The products of the invention have anti-inflammatory, anti-  
 CC autoimmune and anti-diabetic activity. (i), and its (ant)agonists and  
 CC their fragments, are used to treat immune-related diseases, particularly  
 CC T cell-mediated diseases. The diseases treated include systemic lupus  
 CC erythematosus, rheumatoid arthritis, juvenile chronic arthritis,  
 CC spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic  
 CC inflammatory myopathies (dermatomyositis, polymyositis), Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia  
 CC (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune  
 CC thrombocytopenia (idiopathic thrombocytopenic purpura immune-mediated  
 CC thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis,  
 CC juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes  
 CC mellitus, immune-mediated renal disease (glomerulonephritis,  
 CC tubulointerstitial nephritis), multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy, Guillain-Barre syndrome, chronic  
 CC inflammatory demyelinating polyneuropathy, infectious hepatitis  
 CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune  
 CC chronic active hepatitis, primary biliary cirrhosis, granulomatous  
 CC hepatitis, and sclerosing cholangitis, inflammatory bowel disease  
 CC (ulcerative colitis; Crohn's disease), gluten-sensitive enteropathy, and  
 CC Whipple's disease. Autoimmune or immune-mediated skin diseases including  
 CC bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,  
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,  
 CC urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,  
 CC hypersensitivity pneumonitis, and transplantation associated diseases  
 CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists  
 CC or fragment can also be used as an adjuvant in treatment of tumors.  
 CC Antibodies against (I) can also be used for diagnosing such diseases.  
 CC This sequence represents the human PRO245 protein described in the  
 XX invention  
 XX SQ Sequence 312 AA;  
 Query Match 99.2%; Score 385; DB 2; Length 312;  
 Best Local Similarity 97.4%; Pred. No. 5.5e-45;  
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 YHKAYGFSAPKDDQVVAVYQEAILACKTPKTKVSSRLWKLGSRVSFVYVQQTLOGD 60  
 DB 23 YHKAYGFSAPKDDQVVAVYQEAILACKTPKTKVSSRLWKLGSRVSFVYVQQTLOGD 82  
 QY 61 FKRAEMIDFNIRKN 76  
 DB 83 FKRAEMIDFNIRKN 98  
 RESULT 10  
 AAY13354  
 ID AAY13354 standard; protein; 312 AA.  
 XX AC AAY13354;  
 XX DT 25-JUN-1999 (first entry)  
 XX DE Amino acid sequence of protein PRO245.  
 XX KW Secreted protein; transmembrane protein; human; enterocolitis;  
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;  
 KW dermal scarring; Usher Syndrome; Atrophla areata; anti-thrombotic;  
 KW wound healing; tissue repair.  
 XX OS Homo sapiens.  
 XX FN WO9914328-A2.  
 XX PD 25-MAR-1999.  
 XX PF 16-SEP-1998; 98WO-US019330.  
 XX PR 17-SEP-1997; 97US-00591113P.  
 XX PR 17-SEP-1997; 97US-00591155P.  
 XX PR 17-SEP-1997; 97US-0059117P.  
 XX PR 17-SEP-1997; 97US-0059119P.  
 XX PR 17-SEP-1997; 97US-0059121P.  
 XX PR 17-SEP-1997; 97US-0059122P.  
 XX PR 17-SEP-1997; 97US-0059184P.  
 XX PR 18-SEP-1997; 97US-0059263P.  
 XX PR 18-SEP-1997; 97US-0059286P.  
 XX PR 15-OCT-1997; 97US-0082125P.  
 XX PR 15-OCT-1997; 97US-0082285P.  
 XX PR 21-OCT-1997; 97US-0082287P.  
 XX PR 21-OCT-1997; 97US-0083486P.  
 XX PR 24-OCT-1997; 97US-0082814P.  
 XX PR 24-OCT-1997; 97US-0082816P.  
 XX PR 24-OCT-1997; 97US-0083045P.  
 XX PR 24-OCT-1997; 97US-0083120P.  
 XX PR 24-OCT-1997; 97US-0083121P.  
 XX PR 24-OCT-1997; 97US-0083127P.  
 XX PR 24-OCT-1997; 97US-0083128P.  
 XX PR 27-OCT-1997; 97US-0083327P.  
 XX PR 28-OCT-1997; 97US-0083329P.  
 XX PR 28-OCT-1997; 97US-0063541P.  
 XX PR 28-OCT-1997; 97US-0063542P.  
 XX PR 28-OCT-1997; 97US-0063544P.  
 XX PR 28-OCT-1997; 97US-0063549P.  
 XX PR 28-OCT-1997; 97US-0083550P.  
 XX PR 29-OCT-1997; 97US-0083564P.  
 XX PR 29-OCT-1997; 97US-0063704P.  
 XX PR 29-OCT-1997; 97US-0063732P.  
 XX PR 29-OCT-1997; 97US-0063734P.  
 XX PR 29-OCT-1997; 97US-0063735P.  
 XX PR 29-OCT-1997; 97US-0083738P.  
 XX PR 31-OCT-1997; 97US-0064215P.  
 XX PR 31-OCT-1997; 97US-0063870P.  
 XX PR 03-NOV-1997; 97US-0064103P.  
 XX PR 07-NOV-1997; 97US-0064248P.  
 XX PR 12-NOV-1997; 97US-0064809P.  
 XX PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066346P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.  
 XX (GETH ) GENENTECH INC.  
 DA  
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;  
 XX WPI; 1999-229533/19.  
 XX N-PSDB; AAX52225.  
 XX  
 PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT Gastrointestinal ulceration.  
 XX  
 PS Claim 12; Fig 24; 320pp; English.  
 XX  
 CC AAY13344-403 represent secreted and transmembrane human proteins. The  
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal  
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The  
 CC encoded polypeptides have specific uses based on their homology to known  
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated  
 CC with the preservation and maintenance of gastrointestinal mucosa and the  
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,  
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital  
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte  
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous  
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth  
 CC and development, diseases related to growth or survival of nerve cells  
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or  
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal  
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may  
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can  
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may  
 CC have therapeutic applications in wound healing and tissue repair; PRO317  
 CC can be used for treating problems of the kidney, uterus, endometrium,  
 CC blood vessels, or related tissue, e.g. in the heart of genital tract  
 XX  
 SQ Sequence 312 AA;  
 Query Match 99.2%; Score 385; DB 2; Length 312;  
 Best Local Similarity 97.4%; Pred. No. 5.5e-45;  
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YHKAYGFSAPKDOQVTVAXYQEAIIACKTPKTVXSRLEWKLGHSVSVFYVYQOTLQGD 60  
 Db |||||||  
 QY 23 YHKAYGFSAPKDOQVTVAXYQEAIIACKTPKTVXSRLEWKLGHSVSVFYVYQOTLQGD 82  
 Db |||||||  
 QY 61 FKQRAEMIDFNIRIKN 76  
 Db |||||||  
 QY 83 FKQRAEMIDFNIRIKN 98  
 Db |||||||  
 RESULT 11  
 AAB33421  
 ID AAB33421 standard; protein; 312 AA.  
 XX  
 AC AAB33421;  
 XX  
 XX 29-JAN-2001 (first entry)  
 DT  
 XX Human PRO245 protein UNQ0219 SEQ ID NO:36.  
 DE  
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 XX dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neotropic; neuroprotective;  
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease;  
 XX Homo sapiens.  
 XX OS  
 XX PN  
 XX WO2000053758-A2.  
 XX  
 XX 14-SEP-2000.  
 XX  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99US-0123618P.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 23-MAR-1999; 99US-0125775P.  
 PR 12-APR-1999; 99US-0128849P.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 04-MAY-1999; 99US-0132371P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 16-DEC-1999; 99WO-US028565.  
 PR 20-DEC-1999; 99WO-US030095.  
 PR 30-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 99WO-US031274.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 11-FEB-2000; 2000WO-US000376.  
 PR 18-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI; 2000-572271/53.  
 XX N-PSDB; AAC58586.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.  
 XX  
 PS Claim 33; Fig 16; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central and  
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy and whipple's disease, autoimmune  
 CC or immune-mediated skin diseases, allergic diseases, immunological  
 CC diseases of the lung, and transplantation associated diseases including  
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578  
 CC represent PCR primers and hybridisation probes used in the isolation of  
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
 CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 312 AA;

Query Match 99.2%; Score 385; DB 3; Length 312;  
 Best Local Similarity 97.4%; Pred. No. 5.5e-45;  
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQQVVAVXQVEAILLACKTPKTKVXSRLEWKLGSRVSFVYQOQLQGD 60  
 DB 23 YHKAYGFSAPKQQQVVAVXQVEAILLACKTPKTKVXSRLEWKLGSRVSFVYQOQLQGD 82

QY 61 FKNRAEMIDFNIRKN 76  
 DB 83 FKNRAEMIDFNIRKN 98

## RESULT 12

AAV70668  
 ID AAV70668 standard; protein; 312 AA.

XX AC AAY70668;

DT 18-JUL-2000 (first entry)

XX DE Human PRO245 protein.

XX PRO245; UNQ219; dermatological; immunosuppressive; antiinflammatory;  
 KW immunostimulant; antiasthmatic; antirheumatic; antiarthritic; virucide;  
 KW antiallergic; haemostatic; hepatotropic; antidiabetic; antianaeamic;  
 KW nephrotropic; neuroprotective; anticoagulant; immunological disorder;  
 KW lung; pneumonia; skin; psoriasis; kidney; glomerulonephritis; arthritis;  
 KW spondyloarthropathy; SLE; systemic lupus erythematosus; scleroderma;  
 KW idiopathic inflammatory myopathy; anaemia; thrombocytopenia; diabetes;  
 KW thyroiditis; grave's disease; demyelinating disease; multiple sclerosis;  
 KW Crohn's disease; hepatobiliary disease; hepatitis; asthma; human;  
 KW graft-versus-host-disease.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 39..43  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 59..63  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 98..102  
 FT /note= "N-glycosylation site"  
 FT Modified-site 100..104  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 149..153  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 182..188  
 FT /note= "N-myristoylation site"  
 FT Modified-site 187..191

FT Modified-site /note= "N-glycosylation site"  
 FT 205..209  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 226..230  
 FT /note= "Amidation site"  
 FT Modified-site 236..240  
 FT /note= "N-glycosylation site"  
 FT Modified-site 239..245  
 FT /note= "N-myristoylation site"  
 FT Modified-site 255..261  
 FT /note= "N-myristoylation site"  
 FT Modified-site 257..263  
 FT /note= "N-myristoylation site"  
 FT Modified-site 277..281  
 FT /note= "N-glycosylation site"  
 FT Modified-site 284..288  
 FT /note= "Casein Kinase II phosphorylation site"  
 FT Modified-site 305..311  
 FT /note= "N-myristoylation site"

XX WO200015797-A2.

XX PD 23-MAR-2000.

XX PF 15-SEP-1999; 99WO-US021547.

XX PR 17-SEP-1998; 98US-0100858P.

XX PR 17-SEP-1998; 98WO-US019437.

XX PA (GETH) GENENTECH INC.

XX PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;

XX WP1; 2000-271435/23.

XX DR N-PSDB; AA252202.

XX Composition for treatment and diagnosis of immune related diseases e.g.  
 PT Grave's disease comprises a PRO245, PRO217, PRO301, PRO266, PRO335,  
 PT PRO331 or PRO326 polypeptide or its agonists or antagonists (preferably  
 PT antibodies).

PS Example 1; Fig 4; 201pp; English.

XX The present sequence is the human protein PRO245, encoded by UNQ219 cDNA,  
 CC designated as clone DNA35638. It is isolated from human foetal liver  
 CC tissue. It has structural homology to transmembrane protein receptor  
 CC tyrosine kinase family and has 60% amino acid identity with human c-myc  
 CC protein. It enhances or suppresses the infiltration of inflammatory cells  
 CC into tissues, proliferation of T-lymphocytes and modulates the immune  
 CC response. This sequence is useful for treatment of immune related  
 CC disorders, like SLE, rheumatoid/ juvenile arthritis, spondyloarthropathy,  
 CC systemic sclerosis (scleroderma), idiopathic inflammatory myopathies such  
 CC as dermatomyositis, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune haemolytic anaemia, thrombocytopenia, thyroiditis e.g. Grave's  
 CC disease, diabetes mellitus, immune-mediated renal disease e.g.  
 CC glomerulonephritis, demyelinating diseases such as multiple sclerosis and  
 CC Guillain-Barre syndrome, hepatobiliary diseases like hepatitis and  
 CC primary biliary cirrhosis, inflammatory and fibrotic lung diseases such  
 CC as inflammatory bowel disease (e.g. Crohn's disease), autoimmune or  
 CC immune-mediated skin diseases such as psoriasis, allergies like asthma,  
 CC immunological diseases of the lungs such as eosinophilic pneumonia and  
 CC transplantation associated diseases such as graft-versus-host-disease

XX SQ Sequence 312 AA;

Query Match 99.2%; Score 385; DB 3; Length 312;

Best Local Similarity 97.4%; Pred. No. 5.5e-45;

Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQQVVAVXQVEAILLACKTPKTKVXSRLEWKLGSRVSFVYQOQLQGD 60

DB 23 YHKAYGFSAPKQQQVVAVXQVEAILLACKTPKTKVXSRLEWKLGSRVSFVYQOQLQGD 82

QY 61 FKNRAEMIDFNIRIKN 76  
 Db 83 FKNRAEMIDFNIRIKN 98

RESULT 13  
 AAB24401  
 ID AAB24401 standard; protein; 312 AA.  
 XX AC AAB24401;  
 XX DT 07-NOV-2000 (first entry)  
 XX DE Human PRO245 protein sequence SEQ ID NO:67.  
 XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;  
 KW cyostatic; Gene therapy; vaccine.  
 XX OS Homo sapiens.  
 XX PN WO200032221-A2.  
 XX PD 08-JUN-2000.  
 XX PF 30-NOV-1999; 99WO-US028313.  
 XX PR 01-DEC-1998; 98WO-US025108.  
 PR 16-DEC-1998; 98US-0112850P.  
 PR 12-JAN-1999; 99US-0115554P.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99WO-US0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 20-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 28-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 23-OCT-1999; 99US-0162506P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;  
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;  
 PI Smith V, Watanabe CK, Williams PW, Wood WI;  
 XX WPI; 2000-412154/35.  
 DR N-PSDB; AAA77562.  
 XX PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing  
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic  
 PT disorders in mammals.  
 XX PS Claim 72; Fig 28; 315pp; English.  
 XX CC The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the prevention,  
 CC treatment and diagnosis of diseases associated with inappropriate PRO  
 CC expression such as cardiovascular, endothelial or angiogenic disorders in  
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For  
 CC example, the nucleic acids (NCs) and vectors containing them and the PRO  
 CC polypeptide may be used to treat disorders associated with decreased PRO

CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent  
 CC nucleotide and protein sequences used in the exemplification of the  
 CC present invention  
 XX SQ Sequence 312 AA;  
 Query Match 99.2%; Score 385; DB 3; Length 312;  
 Best Local Similarity 97.4%; Pred. No. 5.5e-45;  
 Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YHKAYGFSAPDQDQVVTAVYQEAAILACKTPKTVKSRLEWKLGRSVFVYQOTLQGD 60  
 Db 23 YHKAYGFSAPDQDQVVTAVYQEAAILACKTPKTVKSRLEWKLGRSVFVYQOTLQGD 82  
 QY 61 FKNRAEMIDFNIRIKN 76  
 Db 83 FKNRAEMIDFNIRIKN 98

RESULT 14  
 ADC78384  
 ID ADC78384 standard; protein; 312 AA.  
 XX AC ADC78384;  
 XX DT 01-JAN-2004 (first entry)  
 XX DE Human PRO245 protein.  
 XX KW antiinflammatory; antiulcer; cytostatic; anipsoiratic; antiparkinsonian;  
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;  
 KW antiarteriosclerotic; cardiatic; antidiabetic; cerebroprotective;  
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;  
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;  
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;  
 KW nerve repair; thrombosis; bone; cartilage formation; anglogenesis;  
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;  
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;  
 KW diabetes; stroke; gene therapy; transgenic; PRO; human.  
 XX OS Homo sapiens.  
 XX PN WO200015796-A2.  
 XX PD 23-MAR-2000.  
 XX PF 15-SEP-1999; 99WO-US021090.  
 XX PR 16-SEP-1998; 98WO-US019330.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;  
 PI Yuan J;  
 XX WPI; 2000-271434/23.  
 DR N-PSDB; ADC78383.  
 XX PT Novel nucleic acids encoding secreted and transmembrane polypeptides with  
 PT homology, e.g. to growth and cancer-associated antigens.  
 XX PS Claim 12; SEQ ID NO 64; 355pp; English.  
 XX CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.  
 CC The polypeptides and polynucleotides of the invention may be useful as  
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-  
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,  
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal  
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or  
 CC cartilage formation, anglogenesis, asthma, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,  
 CC infertility, premature aging, AIDS, diabetes complications and stroke.



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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:50:59 ; Search time 5.89305 Seconds  
(without alignments)  
665.797 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388

Sequence: 1 YHKAYGFSAPKDDQVVTAVX.....LQGFKNRAEMIDFNIRKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTCUT COMB.pcp.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	385	99.2	312	4	US-09-254-465A-9
2	385	99.2	312	4	US-09-907-794A-64
3	385	99.2	312	4	US-09-905-125A-64
4	385	99.2	312	4	US-09-902-775A-64
5	384	99.0	298	4	US-09-152-060-76
6	80	20.6	310	4	US-09-907-794A-423
7	80	20.6	310	4	US-09-905-125A-423
8	80	20.6	310	4	US-09-902-775A-423
9	62.5	16.1	213	4	US-09-107-532A-5581
10	59	15.2	602	1	US-08-428-926-5
11	59	15.2	602	1	US-08-428-927-5
12	59	15.2	602	1	US-08-428-298-5
13	59	15.2	602	1	US-08-339-517-5
14	59	15.2	724	4	US-09-562-737-22
15	58.5	15.1	262	4	US-09-328-352-5407
16	58	14.9	121	4	US-09-107-532A-7107
17	57.5	14.8	602	1	US-08-168-091A-2
18	56.5	14.6	115	3	US-08-483-749A-6
19	56.5	14.6	138	2	US-09-057-762-13
20	56.5	14.6	138	2	US-08-326-119A-13
21	56.5	14.6	152	4	US-09-576-594-203
22	56	14.4	354	4	US-09-393-627B-28
23	55.5	14.3	196	4	US-09-328-352-4778
24	55.5	14.3	257	4	US-09-543-681A-6195
25	55	14.2	95	4	US-09-328-352-6933
26	55	14.2	125	2	US-08-039-198B-12
27	55	14.2	125	2	US-08-182-067-2

28	55	14.2	125	2	US-08-465-313-2	Sequence 2, Appli
29	55	14.2	125	4	US-09-809-739-1	Sequence 1, Appli
30	55	14.2	437	4	US-09-252-991A-32414	Sequence 22414, A
31	54.5	14.0	96	4	US-09-489-039A-8700	Sequence 8700, Ap
32	54.5	14.0	296	4	US-09-252-991A-26057	Sequence 26057, A
33	54.5	14.0	488	4	US-09-328-352-4396	Sequence 4396, Ap
34	54.5	14.0	926	4	US-09-543-681A-6681	Sequence 6681, Ap
35	54	13.9	30	4	US-08-948-131-3	Sequence 3, Appli
36	54	13.9	47	2	US-08-310-912A-58	Sequence 58, Appli
37	54	13.9	47	3	US-08-841-089-58	Sequence 58, Appli
38	54	13.9	47	3	US-09-301-085-58	Sequence 58, Appli
39	54	13.9	47	5	PCT-US95-04570-58	Sequence 58, Appli
40	54	13.9	579	4	PCT-US95-04589-58	Sequence 58, Appli
41	54	13.9	670	4	US-09-543-681A-5296	Sequence 5296, Ap
42	54	13.9	105	4	US-09-328-352-6725	Sequence 6725, Ap
43	53.5	13.8	119	4	US-09-497-997C-25	Sequence 25, Appli
44	53.5	13.8	119	4	US-08-875-674A-1	Sequence 1, Appli
45	53.5	13.8	122	4	US-09-556-877-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1

US-09-254-465A-9

; Sequence 9, Application US/09254465A

; Patent No. 6410708

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Napier, Mary A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS

; FILE REFERENCE: P1216R1(US)

; CURRENT APPLICATION NUMBER: US/09/254,465A

; PRIOR FILING DATE: 1999-03-05

; PRIOR APPLICATION NUMBER: PCT/US98/24855

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: US 60/066,364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: US 60/078,936

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: PCT/US98/19437

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 30

; SEQ ID NO 9

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-254-465A-9

Query Match 99.2%; Score 385; DB 4; Length 312;

Best Local Similarity 97.4%; Pred. No. 2e-44; 2; Indels 0; Gaps 0;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVXQEAILACKTPKTVXSRLEWKLGSRVSFVYQQTQD 60

Db 23 YHKAYGFSAPKDDQVVTAVXQEAILACKTPKTVXSRLEWKLGSRVSFVYQQTQD 82

QY 61 FKNRAEMIDFNIRKN 76

Db 83 FKNRAEMIDFNIRKN 98

RESULT 2

US-09-907-794A-64

; Sequence 64, Application US/09907794A

; Patent No. 6635468

Best Local Similarity 97.4%; Pred. No. 2e-44; Indels 0; Gaps 0;  
Matches 74; Conservative 0; Mismatches 2;

QY 1 YHKAYGFSAPKDDQVVTAVYQAEILACKTPKTKVXSRLWKLGSRVSFYVYQQTLOGD 60  
Db 23 YHKAYGFSAPKDDQVVTAVYQAEILACKTPKTKVSSRLWKLGSRVSFYVYQQTLOGD 82

QY 61 FKXRAEMIDFNIRKN 76  
Db 83 FKXRAEMIDFNIRKN 98

RESULT 3  
US-09-905-125A-64  
; Sequence 64, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US/09/905,125A  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02

GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US/09/907,794A  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-09-08  
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; PRIOR APPLICATION NUMBER: PCT/US99/28214  
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; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 64  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-907-794A-64

Query Match 99.2%; Score 385; DB 4; Length 312;



; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-64

Query Match 99.2%; Score 385; DB 4; Length 312;
Best Local Similarity 97.4%; Pred. No. 2e-44;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Dd 23 YHKAYGFSAPKDDQVVTAVXYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQOQTLOGD 82

QY 61 FKNRAEMIDFNIRKN 76
Dd 83 FKNRAEMIDFNIRKN 98.

RESULT 4
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; TITLE OF INVENTION: Acids Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-64

Query Match 99.2%; Score 385; DB 4; Length 312;
Best Local Similarity 97.4%; Pred. No. 2e-44;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVXYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQOQTLOGD 60
Dd 23 YHKAYGFSAPKDDQVVTAVXYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQOQTLOGD 82

QY 61 FKNRAEMIDFNIRKN 76
Dd 83 FKNRAEMIDFNIRKN 98

RESULT 5
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368

APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-125A-423

Query Match 20.6%; Score 80; DB 4; Length 310;
Best Local Similarity 32.0%; Pred. No. 0.0092;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAIIAC-KTPKKTIVSRLEKKL-GRSVSFVYVYQOTIQGDFKNAEMI 68
DB 46 FESVELSCIIITDSQTSDPRIEWKXIQDEQATTVFFDNKIQGDLAQAAIL 95

RESULT 8
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

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; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 5581:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...213
; SEQUENCE DESCRIPTION: SEQ ID NO: 5581:
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; US-09-107-532A-5581
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; Query Match 16.1%; Score 62.5; DB 4; Length 213;
; Best Local Similarity 32.9%; Pred. No. 1.4;
; Matches 25; Conservative 7; Mismatches 19; Indels 25; Gaps 4;
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; QY 11 KDOQVTVAVXQEAIALACKTKPKTVXSRL-EWKK-----LGRSVSVFY 52
; DB 131 KNGKVITA--YSE-----KVDKVVADFLAEWKKTKNEQVKTTVSSQKNESGTGSPSDSG 183
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; QY 53 YQQTLOGDFKNRAEMI 68
; DB 184 SQQTITGSEENQASII 199
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; RESULT 10
; US-08-428-926-5
; Sequence 5, Application US/08428926
; Patent No. 5667780
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osherooff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,926
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339517
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-428-926-5
;
; Query Match 15.2%; Score 59; DB 1; Length 602;
; Best Local Similarity 26.6%; Pred. No. 16;
; Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;
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; QY 11 KDOQVTVAVXQEAIALACKTKPKTVXSRL-EWKKLGRSVSVFYQQTLOGDFKNRAEMIDF 70
; DB 35 KNGEVAVG---OKLVRCETTSYEPALRFKWLKNGKEIT-----KKNRPE----- 76
;
; QY 71 NIRI 74
; DB 77 NVKI 80
;
; RESULT 11
; US-08-428-927-5
; Sequence 5, Application US/08428927
; Patent No. 5756456
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osherooff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,927
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/339517
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-428-926-5

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; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-927-5

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Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

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Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 12
US-08-428-298-5
; Sequence 5, Application US/08428298
; Patent No. 5763213
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osheroff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,298
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-428-298-5

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Best Local Similarity 15.2%; Score 59; DB 1; Length 602;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

Qy 11 KDOQVTVAVXYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGDFKNAEMIDF 70
Db 35 KNOEVAVG---QKLVLCETTSEYPALRFKWLKNGKEIT-----KKNRPE---- 76

Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 13
US-08-339-517-5
; Sequence 5, Application US/08339517
; Patent No. 5770567
; GENERAL INFORMATION:
; APPLICANT: Ho, Wei-Hsien
; APPLICANT: Osheroff, Phyllis L.
; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,517
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-517-5

Query Match
Best Local Similarity 15.2%; Score 59; DB 1; Length 602;
Matches 17; Conservative 12; Mismatches 17; Indels 18; Gaps 3;

Qy 11 KDOQVTVAVXYQEAAILACKTPKTVXSRLEWKLGSRVSFVYQQTLOGDFKNAEMIDF 70
Db 35 KNOEVAVG---QKLVLCETTSEYPALRFKWLKNGKEIT-----KKNRPE---- 76

Qy 71 NIRI 74
Db 77 NVKI 80

RESULT 14
US-09-562-737-22
; Sequence 22, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: US090708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01

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Mon Jul 19 09:51:26 2004

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; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-22

Query Match      15.2%; Score 59; DB 4; Length 724;
Best Local Similarity 28.8%; Pred. No. 20; Indels 24; Gaps 2;
Matches 17; Conservative 5; Mismatches 13; Indels 24; Gaps 2;

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RESULT 15
US-09-328-352-5407
; Sequence 5407, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5407
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5407

Query Match      15.1%; Score 58.5; DB 4; Length 262;
Best Local Similarity 25.0%; Pred. No. 6.4; Indels 19; Gaps 3;
Matches 19; Conservative 12; Mismatches 26; Indels 19; Gaps 3;

Qy      7 PSAPKDDQWTVAV-----XYQEAILACKTPKKTIV-----XSRLWKKLG-RS 47
Db      18 PSAPRYNTLIGVLACVNGVLTFTGLFYQQAIAQDYPIQGFVSHHQENINMKISPOK 77

Qy      48 VSFVYQOTLQDPRN 63
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GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

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1443.181 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388  
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Gapop 10.0 , Gapext 0.5

Searched: 1285345 seqs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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3: /cgn2\_6/ptodata/1/pubaa/US05\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	385	99.2	298	9	US-09-759-777-30
3	385	99.2	298	14	US-10-139-849-2
4	385	99.2	298	14	US-10-192-791-2
5	385	99.2	298	16	US-10-601-953-889
6	385	99.2	312	9	US-09-909-320-64
7	385	99.2	312	9	US-09-909-0888-64
8	385	99.2	312	9	US-09-905-291A-64
9	385	99.2	312	9	US-09-953-499-9
10	385	99.2	312	9	US-09-902-853-64
11	385	99.2	312	9	US-09-907-824-64
12	385	99.2	312	9	US-09-907-841-64
13	385	99.2	312	10	US-09-904-011-64
14	385	99.2	312	10	US-09-906-742-64
15	385	99.2	312	10	US-09-906-838-64

16	385	99.2	312	10	US-09-907-613-64	Sequence 64, Appl
17	385	99.2	312	10	US-09-907-942-64	Sequence 64, Appl
18	385	99.2	312	10	US-09-904-859-64	Sequence 64, Appl
19	385	99.2	312	10	US-09-909-204-64	Sequence 64, Appl
20	385	99.2	312	10	US-09-904-820-64	Sequence 64, Appl
21	385	99.2	312	10	US-09-904-786-64	Sequence 64, Appl
22	385	99.2	312	10	US-09-906-646-64	Sequence 64, Appl
23	385	99.2	312	10	US-09-906-700-64	Sequence 64, Appl
24	385	99.2	312	10	US-09-903-786-64	Sequence 64, Appl
25	385	99.2	312	10	US-09-902-903-64	Sequence 64, Appl
26	385	99.2	312	10	US-09-903-749A-64	Sequence 64, Appl
27	385	99.2	312	10	US-09-904-119-64	Sequence 64, Appl
28	385	99.2	312	10	US-09-904-856-64	Sequence 64, Appl
29	385	99.2	312	10	US-09-902-736-64	Sequence 64, Appl
30	385	99.2	312	10	US-09-907-794-64	Sequence 64, Appl
31	385	99.2	312	10	US-09-903-943-64	Sequence 64, Appl
32	385	99.2	312	10	US-09-904-462-64	Sequence 64, Appl
33	385	99.2	312	10	US-09-907-925-64	Sequence 64, Appl
34	385	99.2	312	10	US-09-902-892-64	Sequence 64, Appl
35	385	99.2	312	10	US-09-903-520-64	Sequence 64, Appl
36	385	99.2	312	10	US-09-905-056-64	Sequence 64, Appl
37	385	99.2	312	10	US-09-909-064-64	Sequence 64, Appl
38	385	99.2	312	10	US-09-904-553-64	Sequence 64, Appl
39	385	99.2	312	10	US-09-905-381-64	Sequence 64, Appl
40	385	99.2	312	10	US-09-905-088-64	Sequence 64, Appl
41	385	99.2	312	10	US-09-907-575-64	Sequence 64, Appl
42	385	99.2	312	10	US-09-905-075-64	Sequence 64, Appl
43	385	99.2	312	10	US-09-902-759-64	Sequence 64, Appl
44	385	99.2	312	10	US-09-902-634-64	Sequence 64, Appl
45	385	99.2	312	10	US-09-902-713-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1

US-09-745-763-38

; Sequence 38, Application US/09745763

; Patent No. US20020065394A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; Lavallie, Edward R.

; Collins-Racie, Lisa A.

; Evans, Cheryl

; Merberg, David

; Treacy, Maurice

; Spaulding, Vikki

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 219

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/745,763

; FILING DATE: 18-Jun-2000

; CLASSIFICATION: <UNKNOWN>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne A.

; REGISTRATION NUMBER: 41,323

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-745-763-38

Query Match 99.2%; Score 385; DB 9; Length 298;  
Best Local Similarity 97.4%; Pred. No. 9.6e-43;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 60  
DB 23 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 82  
QY 61 FKNRAEMIDFNIRIKN 76  
DB 83 FKNRAEMIDFNIRIKN 98

RESULT 2  
US-09-799-777-30  
Sequence 30, Application US/09799777  
Patent No. US20020091244A1  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
Hillman, Jennifer L.  
Corley, Neil C.  
Guegler, Karl J.  
Baugh, Mariah  
Sather, Susan  
Shah, Purvi  
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 154  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,777  
FILING DATE: 06-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,485  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BILLINGS, LUCY J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0459 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: DUODN02  
CLONE: 1704050  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-799-777-30

Query Match 99.2%; Score 385; DB 9; Length 298;  
Best Local Similarity 97.4%; Pred. No. 9.6e-43;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 60  
DB 23 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 82  
QY 61 FKNRAEMIDFNIRIKN 76  
DB 83 FKNRAEMIDFNIRIKN 98

RESULT 3  
US-10-139-849-2  
Sequence 2, Application US/10139849  
Publication No. US20030079238A1  
GENERAL INFORMATION:  
APPLICANT: Cunningham, Sonia  
Barros, Maria Pia  
TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN  
JUNCTIONAL ADHESION PROTEIN (JAM 2)  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROCKEY, MILNAMOW & KATZ, LTD.  
STREET: 180 N. STETSON AVENUE, 2 PRUDENTIAL PLAZA,  
SUITE 4700  
CITY: CHICAGO  
STATE: IL  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/139,849  
FILING DATE: 07-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,929  
FILING DATE: 23-Aug-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25,011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-139-849-2

Query Match 99.2%; Score 385; DB 14; Length 298;  
Best Local Similarity 97.4%; Pred. No. 9.6e-43;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 60  
DB 23 YHKAYGFSAPKDDQVVTAVYQAEAILACKTPKKTIVSRLEWKLGSRVSFVYQQTLOGD 82  
QY 61 FKNRAEMIDFNIRIKN 76  
DB 83 FKNRAEMIDFNIRIKN 98



## RESULT 4

US-10-192-791-2  
; Sequence 2, Application US/10192791  
; Publication No. US20030130166A1  
; GENERAL INFORMATION:  
; APPLICANT: Texas Biotechnology Corporation  
; TITLE OF INVENTION: A Polynucleotide Encoding a Human Junctional Adhesion Protein (JAP)  
; FILE REFERENCE: TEX4542P0430  
; CURRENT APPLICATION NUMBER: US/10/192,791  
; CURRENT FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-192-791-2

Query Match 99.2%; Score 385; DB 14; Length 298;  
Best Local Similarity 97.4%; Pred. No. 9.6e-43;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1 YHKAIGFSAPKDDQVVTAIVYQEAAILACKTPKKTIVXSRLWKLGSRVSFVYVYQTLQGD 60
Db	
23 YHKAIGFSAPKDDQVVTAIVYQEAAILACKTPKKTIVXSRLWKLGSRVSFVYVYQTLQGD 82	
QY	61 FKRAEMIDFNIRIKN 76
Db	
83 FKRAEMIDFNIRIKN 98	

## RESULT 5

US-10-601-953-889  
; Sequence 889, Application US/10601953  
; Publication No. US20040077540A1  
; GENERAL INFORMATION:  
; APPLICANT: Quav, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial  
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of  
; TITLE OF INVENTION: Therapeutic Compounds  
; FILE REFERENCE: 02-03US  
; CURRENT APPLICATION NUMBER: US/10/601,953  
; CURRENT FILING DATE: 2003-06-24  
; PRIOR APPLICATION NUMBER: 60/392,512  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 889  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-601-953-889

Query Match 99.2%; Score 385; DB 16; Length 298;  
Best Local Similarity 97.4%; Pred. No. 9.6e-43;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1 YHKAIGFSAPKDDQVVTAIVYQEAAILACKTPKKTIVXSRLWKLGSRVSFVYVYQTLQGD 60
Db	
23 YHKAIGFSAPKDDQVVTAIVYQEAAILACKTPKKTIVXSRLWKLGSRVSFVYVYQTLQGD 82	
QY	61 FKRAEMIDFNIRIKN 76
Db	
83 FKRAEMIDFNIRIKN 98	

## RESULT 6

US-09-909-320-64  
; Sequence 64, Application US/09909320  
; Patent No. US20020132240A1  
; GENERAL INFORMATION:

Query Match 99.2%; Score 385; DB 9; Length 312;  
Best Local Similarity 97.4%; Pred. No. 1e-42;

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,320  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 64  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-909-320-64

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: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR PCT NO.: 99/30911
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423

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TYPE: PRI  
ORGANISM: Homo sapiens  
US-09-909-088B-64

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Query Match      99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels
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Query Match      99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-4;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 YHKAYGFSAPKQQQVTVAYVEYGEAILACKTPKTKTVXSRLEWKKLGSRVSFVYVQCTIQGD 60
QY

23 YHKAYGFSAPKDDQWTVAYVEYGEAILACKTPKTKTVXSRLEWKKLGSRVSFVYVQCTIQGD 82
DB

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RESULT 3  
US-09-905-291A-64  
; Sequence 64. Application US/09905291A

US-03-905-291A-64  
; Sequence 64, Application US/09050291A  
; Patent No. US20020160374A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.

/ APPLICANT: Goddard, A.  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth, J.  
 / APPLICANT: Khlavin, Ivan J.  
 / APPLICANT: Mather, Jennie P.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William, I.  
 / TITLE OF INVENTION: Secreted and Transmembrane  
 / FILE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: 10466-14  
 / CURRENT APPLICATION NUMBER: US/09/905,291A  
 / CURRENT FILING DATE: 2001-07-12  
 / PRIOR APPLICATION NUMBER: PCT/US00/04414  
 / PRIOR FILING DATE: 2000-02-22  
 / PRIOR APPLICATION NUMBER: US 60/143,048  
 / PRIOR FILING DATE: 1999-07-07  
 / PRIOR APPLICATION NUMBER: US 60/145,698  
 / PRIOR FILING DATE: 1999-07-26  
 / PRIOR APPLICATION NUMBER: US 60/146,222  
 / PRIOR FILING DATE: 1999-07-28  
 / PRIOR APPLICATION NUMBER: PCT/US99/20594  
 / PRIOR FILING DATE: 1999-09-08  
 / PRIOR APPLICATION NUMBER: PCT/US99/20994

Polymetides and Nucleic

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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-64

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQOTLQGD 60
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQOTLQGD 82

QY 61 FKNRAEMIDFNIRKN 76
DB 83 FKNRAEMIDFNIRKN 98

RESULT 9
US-09-953-499-9
; Sequence 9, Application US/09953499
; Publication No. US20020182206A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; OF DISEASES CHARACTERIZED BY A33 - RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/953,499
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-9

Query Match          99.2%; Score 385; DB 9; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQOTLQGD 60
DB 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKTVKSRLWKLGSRVSFVYVYQOTLQGD 82

QY 61 FKNRAEMIDFNIRKN 76
DB 83 FKNRAEMIDFNIRKN 98

RESULT 10
US-09-902-853-64
; Sequence 64, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS ENCODING THE SAME
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
```



APPLICANT: KJlavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,841  
CURRENT FILING DATE: 2001-11-20  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-09-08  
PRIOR FILING DATE: 1999-09-13  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-11-29  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 64  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-907-841-64

Query Match  
Best Local Similarity 99.2%; Score 385; DB 9; Length 312;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQVTVAVYQAEAILACKTPKKTVXSRLWKLGSRVSFVYQQTLQGD 60  
23 YHKAYGFSAPKQQVTVAVYQAEAILACKTPKKTVSSRLWKLGSRVSFVYQQTLQGD 82

Db 61 FKRAEMIDFNIRIKN 76  
83 FKRAEMIDFNIRIKN 98

QY 61 FKRAEMIDFNIRIKN 76  
83 FKRAEMIDFNIRIKN 98

Db 61 FKRAEMIDFNIRIKN 76  
83 FKRAEMIDFNIRIKN 98

RESULT 13  
US-09-904-011-64  
Sequence 64, Application US/09904011  
Publication No. US2003003530A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: KJlavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,011  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 64  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-011-64

Query Match  
Best Local Similarity 99.2%; Score 385; DB 10; Length 312;  
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKQQVTVAVYQAEAILACKTPKKTVXSRLWKLGSRVSFVYQQTLQGD 60  
23 YHKAYGFSAPKQQVTVAVYQAEAILACKTPKKTVSSRLWKLGSRVSFVYQQTLQGD 82

Db 61 FKRAEMIDFNIRIKN 76  
83 FKRAEMIDFNIRIKN 98

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RESULT 14
US-09-906-742-64
; Sequence 64, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-15
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64

RESULT 15
US-09-906-838-64
; Sequence 64, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-64
Query Match 99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 60
Db 23 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 82
QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-64
Query Match 99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 60
Db 23 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 82
QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-64
Query Match 99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 60
Db 23 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 82
QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-64
Query Match 99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred. No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 60
Db 23 YHAYGFSAPKDDQVVTAVYQAEILACKTPKTVXSELEWKLGRSVSFVYVQOTLQGD 82
QY 61 FKNRAEMIDFNIRKN 76
Db 83 FKNRAEMIDFNIRKN 98
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-64

Query Match          99.2%; Score 385; DB 10; Length 312;
Best Local Similarity 97.4%; Pred.No. 1e-42;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSRLEWKLGSRVSFVYYQQTLOGD 60
Db 23 YHKAYGFSAPKDDQVVTAVYQEAAILACKTPKKTVXSRLEWKLGSRVSFVYYQQTLOGD 82

QY 61 FKRAEMIDFNIRIKN 76
Db 83 FKRAEMIDFNIRIKN 98
```

Search completed: July 16, 2004, 00:03:55  
Job time : 16.4599 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:58 ; Search time 5.6984 Seconds  
(without alignments)  
1284.844 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388  
Sequence: 1 YKAYGSPAKDQVWVAVX.....LQDFKNRAEMIDFNIRKN 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	17.0	157	2 PH0201	hypothetical prote
2	64	16.5	760	2 T28224	ORF MSV063 probabl
3	62	16.0	231	2 S45089	hypothetical prote
4	60.5	15.6	156	2 D86704	transcription elon
5	60.5	15.6	188	2 A11062	phage polarity sup
6	60.5	15.6	246	2 A32293	holliday junction
7	60.5	15.6	1526	2 JN0598	DNA topoisomerase
8	60	15.5	124	2 C97871	hypothetical prote
9	59.5	15.3	346	2 A96270	ruvB, holliday jun
10	59.5	15.3	346	2 AF3014	Holliday junction
11	59.5	15.3	414	2 A12823	aminotransferase [
12	59.5	15.3	414	2 H97601	hypothetical prote
13	59.5	15.3	444	2 A20645	hypothetical prote
14	59.5	15.3	803	2 H11839	flagellar function
15	59.5	15.3	1584	2 F96573	protein Fl2M16.25
16	59	15.2	433	2 S26646	transcription fact
17	59	15.2	602	2 A45769	acetylcholine rece
18	58.5	15.1	301	2 A11635	C. perfringens tra
19	58.5	15.1	333	2 AP2084	ABC transporter, p
20	58.5	15.1	534	2 B44590	hypothetical prote
21	58	14.9	224	2 T45922	hypothetical prote
22	58	14.9	586	2 A2065	hypothetical prote
23	58	14.9	949	2 H97322	DNA/RNA helicase,
24	57.5	14.8	117	1 HVMS39	IG heavy chain pre
25	57.5	14.8	119	2 D27889	IG heavy chain V r
26	57.5	14.8	148	2 G83681	urease accessory p
27	57.5	14.8	323	2 B22943	probable ABC subst
28	57.5	14.8	623	2 S46427	botulinum neurotox
29	57.5	14.8	706	2 F82148	methyl-accepting c

30	57.5	14.8	848	2 C70203	DNA topoisomerase
31	57.5	14.8	1084	2 B64058	hemoglobin-binding
32	57.5	14.8	1526	2 A44406	DNA topoisomerase
33	57.5	14.8	1528	2 A44406	DNA topoisomerase
34	57	14.7	138	1 BGRU2	spermatid transiti
35	57	14.7	300	2 S76881	hypothetical prote
36	57	14.7	321	2 A64173	conserved hypotet
37	57	14.7	599	2 D70104	DNA topoisomerase
38	57	14.7	641	2 T50091	succinate dehydrog
39	57	14.7	868	2 D86349	hypothetical prote
40	57	14.7	1386	2 T00257	hypothetical prote
41	56.5	14.6	218	2 A33136	proline/arginine-r
42	56.5	14.6	976	1 TVMSMD	macrophage colony-
43	56.5	14.6	1530	2 A40493	DNA topoisomerase
44	56	14.4	589	2 I38598	zinc finger protei
45	56	14.4	810	1 S50889	PRK1 protein - yea

## ALIGNMENTS

### RESULT 1

PH0201  
hypothetical protein 157 - Enterococcus faecalis plasmid pAM-beta-1 (fragment)  
C:Species: Enterococcus faecalis  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jul-2000  
C:Accession: PH0201  
R:Winfield, R.J.; Oultram, J.D.; Thompson, D.E.; Brehm, J.K.; Minton, N.P.  
Gene 87, 79-90, 1990

A:Title: Physical characterisation of the replication region of the Streptococcus faecali  
A:Reference number: PH0201; MUID:90236302; PMID:2110101

A:Accession: PH0201

A:Molecule type: DNA

A:Residues: 1-157 <SWI>

A:Cross-references: EMBL:X17092; NID:93023041; PIDN:AAC38598.1; PID:93023042

C:Genetics:

A:Genome: plasmid

C:Keywords: plasmid replication

Query Match 17.0%; Score 66; DB 2; Length 157;  
Best Local Similarity 24.4%; Pred. No. 1.3;

Matches 21; Conservative 17; Mismatches 26; Indels 22; Gaps 4;

QY 1 YKAYGSPAKDQVWVAVXYQEAAILACKTPKTVXSRLEWKKLGRSVSVFY---QOTL 57  
DB 59 YELTYFQEKXQ---NYQSLRTYVSEKVDIS---DWKALGKTLKSVNYGSEQTK 110  
QY 58 QG-----DFKNRAEMIDFNI 72  
DB 111 KGYSVEYLLNVSDNRSKWQKITFEV 136

### RESULT 2

T28224  
ORF MSV063 probable early transcription factor large subunit homolog VETF-L (vaccinia A71  
C:Species: Melanoplus sanguinipes entomopoxvirus  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T28224  
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.P.; Rock, D.L.  
J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28224

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-760 <AFO>

A:Cross-references: EMBL:AF063866; NID:G4049647; PIDN:AAC97622.1; PID:G4049662

C:Genetics:

A>Note: MSV063

Query Match 16.5%; Score 64; DB 2; Length 760;

Best Local Similarity 27.1%; Pred. No. 13;

Matches 23; Conservative 10; Mismatches 34; Indels 18; Gaps 3;

QY 10 PKQQVVTVAYXQ---EAILACKTPKTKVXSRLEWKKLGRSVSFVYQOTLQGDFFKRAE 66  
 DB 119 PNDKSLYNIYQIVGAVFCVTTNKNGSQLARSNVYSSVYRDYISEIINNIYKNRYA 178  
 QY 67 M-----IDFN--IRIKN 76  
 DB 179 MKSSIIDAMEYSINIDFQDLRLRN 203  
 RESULT 3  
 S45089  
 hypothetical protein eta - Streptococcus pyogenes plasmid pDB101  
 C:Species: Streptococcus pyogenes  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 15-Oct-1999  
 C:Accession: S68123; S45089  
 R:Ceglowski, P.; Alonso, J.C.  
 Gene 145, 33-39, 1994  
 A:Title: Gene organization of the Streptococcus pyogenes plasmid pDB101: sequence analysis  
 A:Reference number: S68123; MUID:94320784; PMID:8093174  
 A:Accession: S68123  
 A:Molecule type: DNA  
 A:Residues: 1-231 <CE2>  
 A:Cross-references: EMBL:X66468; NID:9436500; PIDN:CAA47095.1; PID:S559958  
 A:Experimental source: plasmid pDB101  
 C:Genetics:  
 A:Genome: plasmid pDB101  
 A:Start codon: TTG  
 Query Match 16.0%; Score 62; DB 2; Length 231;  
 Best Local Similarity 23.3%; Pred. No. 6.2; Mismatches 26; Indels 22; Gaps 4;  
 Matches 20; Conservative 18  
 QY 1 YKAYGFSAPKQQVVTVAYXQAEAILACKTPKTKVXSRLEWKKLGRSVSFVY---QOTL 57  
 DB 133 YFLTYYFQSKNGE-----NYQSSLTYYVSEKVDIS---DMKALGKTLKSNVYVYSGEQTK 184  
 QY 58 QG-----DFKNRAEMIDFNI 72  
 DB 185 KGYSVEYLLNVTVEDRSKQKXITFEV 210  
 RESULT 4  
 D86704  
 transcription elongation factor GreA greA [imported] - Lactococcus lactis subsp. lactis  
 C:Species: Lactococcus lactis subsp. lactis  
 C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: D86704  
 R:Belotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: D86704  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-156 <SFO>  
 A:Cross-references: GB:AE005176; PID:gi2723539; PIDN:AAK04734.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: greA  
 C:Superfamily: transcription elongation factor greb  
 C:Keywords: transcription factor  
 Query Match 15.6%; Score 60.5; DB 2; Length 156;  
 Best Local Similarity 26.1%; Pred. No. 6.2; Mismatches 28; Indels 25; Gaps 4;  
 Matches 24; Conservative 15  
 QY 3 KAYG-----FSAPKQQO-----VTVAVXYQAEAILACKTPKTKVXSRLEWKKLGR 46  
 DB 38 RSYGDLSENSEYEAADKQAEFEGRISTVETMIRVAEIVDNAKIAQDEVA-----LGK 90  
 QY 47 SVSFVYQOTLQGDFFK---NEAEMIDFNIRKN 76  
 DB 185 KGYSVEYLLNVTVEDRSKQKXITFEV 210  
 RESULT 5  
 AF1062  
 phage polarity suppression protein [imported] - Salmonella enterica subsp. enterica serov. typhi  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AF1062  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Garra, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov.  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AF1062  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-188 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD06947.1; PID:gl6505594; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STI4825  
 C:Superfamily: phage P4 amber mutation-suppressing protein  
 Query Match 15.6%; Score 60.5; DB 2; Length 188;  
 Best Local Similarity 34.9%; Pred. No. 7.6; Mismatches 26; Indels 7; Gaps 3;  
 Matches 22; Conservative 8  
 QY 16 VTAVXYQAEAILACKTPKTKVXSRLEWKKLGRSVSFVYQOTLQGDFFKRAEMIDF--NI 72  
 DB 1 MTTVTIQAFACQTNKNTWLKRAELADLERE---YREQLLAGDEQIPRRMQDLRDNI 56  
 QY 73 RIK 75  
 DB 57 DVK 59  
 RESULT 6  
 AH3293  
 holliday junction DNA helicase ruvB [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002  
 C:Accession: AH3293  
 R:DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.;  
 Maer, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AB3252; PMID:11756688  
 A:Accession: AH3293  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-346 <KJB>  
 A:Cross-references: GB:AE008917; PIDN:AAL51515.1; PID:gl7982230; GSPDB:GN00190  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI0334  
 A:Map position: I  
 C:Superfamily: ruvB protein  
 Query Match 15.6%; Score 60.5; DB 2; Length 346;  
 Best Local Similarity 28.3%; Pred. No. 15; Mismatches 29; Indels 3; Gaps 2;  
 Matches 17; Conservative 11  
 QY 4 AVGFSAPKQ---QQVVTVAVXYQAEAILACKTPKTKVXSRLEWKKLGRSVSFVYQOTLQGDFF 61  
 DB 284 AAGLSEPRDAIEDIEPYLIQQQFLQ-RTPGRVLTAVAMQHLGPAPAEIQQSQYGLF 342  
 RESULT 7  
 JN0598  
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - rat

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* 294, 2323-2328, 2001

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: A96270

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-346 <KUR>

A:CROSS-references: GB:AE007870; PIDN:AAK89683.1; PID:g15159589; GSPDB:GN00170

C:Genetics:

A:Gene: AGR\_L.2225

A:Map position: linear chromosome

C:Superfamily: ruvB protein

Query Match 15.3%; Score 59.5; DB 2; Length 346;  
Best Local Similarity 23.8%; Pred. No. 19;  
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;

QY 4 AYGFSA PKD--QQVTVAVXYQCEAILACKTPKTVXSLEWKKLG----RSVSFVYVYQOTL 57  
DB 285 AAGLSEPRDAIEDIIEPYMIQQGFIQ-RTPRGRILTATANKHGLQPPKDLAAQFRFLT 343  
QY 58 QGD 60  
DB 344 EDD 346

RESULT 10  
AF3014  
Holliday junction DNA helicase RuvB [imported] - *Agrobacterium tumefaciens* (strain C58, I  
C:Species: *Agrobacterium tumefaciens*  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AF3014  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan  
; Karp, P.; Romero, P.; Zhang, S.  
Science 284, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.  
ster, E.W.  
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF3014  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-346 <KUR>  
A:CROSS-references: GB:AE008689; PIDN:AAU44532.1; PID:g17742145; GSPDB:GN00187  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: ruvB  
A:Map position: linear chromosome  
C:Superfamily: ruvB protein

Query Match 15.3%; Score 59.5; DB 2; Length 346;  
Best Local Similarity 23.8%; Pred. No. 19;  
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;

QY 4 AYGFSA PKD--QQVTVAVXYQCEAILACKTPKTVXSLEWKKLG----RSVSFVYVYQOTL 57  
DB 285 AAGLSEPRDAIEDIIEPYMIQQGFIQ-RTPRGRILTATANKHGLQPPKDLAAQFRFLT 343  
QY 58 QGD 60  
DB 344 EDD 346

RESULT 11  
AI2823  
aminotransferase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)  
C:Species: *Agrobacterium tumefaciens*  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AI2823  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan  
; Karp, P.; Romero, P.; Zhang, S.  
Science 284, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.  
ster, E.W.  
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF3014  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-346 <KUR>  
A:CROSS-references: GB:AE008689; PIDN:AAU44532.1; PID:g17742145; GSPDB:GN00187  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: ruvB  
A:Map position: linear chromosome  
C:Superfamily: ruvB protein

; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AI2823  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-414 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AAL43007.1; PID:gl7740470; GSPDB:GN00186  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu2015  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli valine-pyruvate transaminase  
 Query Match 15.3%; Score 59.5; DB 2; Length 414;  
 Best Local Similarity 30.6%; Pred. No. 23;  
 Matches 26; Conservative 7; Mismatches 29; Indels 23; Gaps 4;  
 QY 7 FSAPKQQVTVAVXQEAIIAC-----KTPKKTVXSRLEWKKLGRSVSFV 51  
 DB 115 FUSPKDTALTVTWPTLYGALSANVAYEPNYDQLNPGGNRTPE---AYRETAAKLGGAVKFA 171  
 QY 52 YVQOTLQGDFFKN-RAEMIDFNIRIK 75  
 DB 172 Y----LSADFSNPTGETVDLAGREK 192  
 RESULT 12  
 H97601  
 hypothetical protein AGR\_C\_3654 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
 C:Accession: H97601  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: H97601  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-414 <KUR>  
 A:Cross-references: GB:AE007869; PIDN:AAK87769.1; PID:gi5157139; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C\_3654  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli valine-pyruvate transaminase  
 Query Match 15.3%; Score 59.5; DB 2; Length 414;  
 Best Local Similarity 30.6%; Pred. No. 23;  
 Matches 26; Conservative 7; Mismatches 29; Indels 23; Gaps 4;  
 QY 7 FSAPKQQVTVAVXQEAIIAC-----KTPKKTVXSRLEWKKLGRSVSFV 51  
 DB 115 FUSPKDTALTVTWPTLYGALSANVAYEPNYDQLNPGGNRTPE---AYRETAAKLGGAVKFA 171  
 QY 52 YVQOTLQGDFFKN-RAEMIDFNIRIK 75  
 DB 172 Y----LSADFSNPTGETVDLAGREK 192  
 RESULT 13  
 AE0646  
 hypothetical protein STY1268 [imported] - Salmonella enterica subsp. enterica serovar Ty  
 C:Species: Salmonella enterica subsp. enterica serovar typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AE0646  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

A;Accession: F96573  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1584 <STO>  
A;Cross-references: GB:AE005173; NID:g7769860; PIDN:AAF69538.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: FL2M16.25  
A;Map position: 1

Query Match 15.3%; Score 59.5; DB 2; Length 1584;  
Best Local Similarity 25.3%; Pred. No. 98;  
Matches 20; Conservative 13; Mismatches 25; Indels 21; Gaps 3;

Qy 9 APKDQOVTVAVXYQEI-----LACKTPKTVXSELEWKLGSRVSFVYQOTL----- 57  
Db 70 SPKVDNVVILDHHTAIDSLGVS LTC-----KNVTSVLDIERSGATIAFDYFQKLVEES 125

Qy 58 -----QGDFKNRAEMIDF 70  
Db 126 RGSCKENNDFKMRVFEX 144

Search completed: July 15, 2004, 23:55:08  
Job time : 6.68984 secs



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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:03 ; Search time 3 25134 Seconds

(without alignments)  
1217.140 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388

Sequence: 1 YHKAYGFSAPKQDVVAVX.....LQDFKNRAEMIDFIRIKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	93.2	298	1	JAM2 HUMAN
2	64	16.5	760	1	Q9YV29 melanophilus
3	62.5	16.1	346	1	RUVB_RHIME
4	62.5	16.1	500	1	SVE_LACDE
5	60.5	15.6	156	1	GREA_LACLA
6	60.5	15.6	346	1	RUVB_BRUME
7	60.5	15.6	346	1	RUVB_BRUSU
8	60.5	15.6	1526	1	TP2A_RAT
9	60	15.5	1076	1	CARB_BUCBP
10	59.5	15.3	346	1	RUVB_AGRFS
11	59	15.2	602	1	NRG1_CHICK
12	57.5	14.8	117	1	HV59_MOUSE
13	57.5	14.8	346	1	RUVB_RHIE
14	57.5	14.8	470	1	YPC2_CAEEL
15	57.5	14.8	623	1	HA70_CLOBO
16	57.5	14.8	848	1	TOP1_BORBU
17	57.5	14.8	1065	1	HQBP_HABIN
18	57.5	14.8	1067	1	HQBP_HABIN
19	57.5	14.8	1084	1	HQBP_HABIN
20	57.5	14.8	1526	1	TP2A_CRIGR
21	57.5	14.8	1528	1	TP2A_MOUSE
22	57	14.7	138	1	TP2A_HUMAN
23	57	14.7	313	1	ISPE_HABIN
24	57	14.7	599	1	PARE_BORBU
25	57	14.7	641	1	DHSA_SCHPO
26	56.5	14.6	1531	1	TP2A_HUMAN
27	56.5	14.6	1533	1	TP2A_PIG
28	56	14.4	589	1	2132_HUMAN
29	56	14.4	810	1	KIJ5_YEAST
30	55.5	14.3	506	1	SHS1_BOVIN
31	55.5	14.3	551	1	CHIT_NPVAC
32	55.5	14.3	1323	1	ADRI_YEAST
33	55	14.2	79	1	CKS2_XENLA

#### ALIGNMENTS

##### RESULT 1

ID	JAM2_HUMAN	STANDARD	PRT	298 AA
AC	P57087			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Junctional adhesion molecule 2 precursor (Vascular endothelial			
DE	junction-associated molecule) (VE-JAM)			
GN	JAM2 OR VEJAM OR C21ORP43			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Vascular endothelial cells;			
RX	MEDLINE=20317114; PubMed=10779521;			
RA	Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;			
RT	"Vascular endothelial junction-associated molecule, a novel member of			
RT	the immunoglobulin superfamily, is localized to intercellular			
RT	boundaries of endothelial cells."			
RL	J. Biol. Chem. 275:19139-19145(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=20507930; PubMed=10945976;			
RA	Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,			
RA	Vanderslice P., Morris A.P., Brock T.A.;			
RT	"A novel protein with homology to the junctional adhesion molecule:			
RT	Characterization of leukocyte interactions."			
RL	J. Biol. Chem. 275:34750-34756(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,			
RA	Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

Q9ku18 vibrio chol  
P27472 saccharomyc  
Q09737 schizosacch  
P42424 bacillus su  
Q00495 rattus norv  
P12174 marcantia  
O40619 human papil  
P25979 xenopus lae  
P37297 saccharomyc  
O50632 bacillus ha  
Q92766 chlamydia p  
P55407 rhizobium s





```
CC -!- SIMILARITY: Belongs to the ruvB family.
CC -----
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CC -----
CC
CC DR EMBL; AL591791; CAC47328.1; -.
CC DR HAMAP; MF_00016; -.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR InterPro; IPR003959; AAA_ATPase_cent.
CC DR InterPro; IPR004605; RuvB.
CC DR InterPro; IPR008823; RuvB_C.
CC DR InterPro; IPR008824; RuvB_N.
CC DR Pfam; PF00004; AAA; 1.
CC DR Pfam; PF05491; RuvB_C; 1.
CC DR Pfam; PF05496; RuvB_N; 1.
CC DR SMART; SM00382; AAA; 1.
CC DR TIGRFAMs; TIGR00635; ruvB; 1.
CC DR DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
CC KW Complete proteome.
CC FT NP BIND 60 67 ATP (POTENTIAL).
CC SQ SEQUENCE 346 AA; 38180 MW; 50EDD2C1EDA6CDC6 CRC64;
CC
CC Query Match 16.1%; Score 62.5; DB 1; Length 346;
CC Best Local Similarity 28.6%; Pred. No. 3.4;
CC Matches 18; Conservative 12; Mismatches 26; Indels 7; Gaps 3;
CC
CC QY 4 AYGFSAFKD--QQVTVAVYQEAAILACKPKTKVXSRLEWKKLG-----RSVSFVYQQQL 57
CC Db 285 AAGLSEPRDAIEDIEPYLIQQGFIO-RTPRGRVLTANAWKHGLNPPRPDRDVEASQFRLTL 343
CC
CC QY 58 QGD 60
CC Db 344 EDD 346
CC
CC RESULT 4
CC SYE_LACDE STANDARD; PRT; 500 AA.
CC AC 086083;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Glutanyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
CC DE (GluRS).
CC GN GLTX.
CC OS Lactobacillus delbrueckii (subsp. bulgaricus).
CC OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
CC OC Lactobacillus.
CC OX NCBI_TaxID=1585;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Ishino Y., Kim S.I., Soell D.;
CC RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC phosphate + L-glutamyl-tRNA(Glu).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
CC
CC DR EMBL; AF084366; AAC32611.1; -.
CC DR HAMAP; MF_00105; -.
CC
CC HSSP; P27000; IGLN.
CC HAMAP; MF_00022; -.
CC InterPro; IPR004527; Gltx_bact.
CC InterPro; IPR000924; Glu_tRNA-synt_1c.
CC InterPro; IPR008925; tRNA-synt_bind.
CC InterPro; IPR001412; tRNA-synt_1.
CC Pfam; PF00749; tRNA-synt_1c; 1.
CC PRINTS; PR00987; TRNASYNTHGLU.
CC TIGRFAMs; TIGR00464; gltx_bact; 1.
CC PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
CC FT SITE 12 22 "HIGH" REGION.
CC FT SITE 259 263 "KMSKS" REGION.
CC FT BINDING 262 262 ATP (BY SIMILARITY).
CC SQ SEQUENCE 500 AA; 56944 MW; 30EAA09133AE6841 CRC64;
CC
CC Query Match 16.1%; Score 62.5; DB 1; Length 500;
CC Best Local Similarity 22.1%; Pred. No. 5.1;
CC Matches 15; Conservative 12; Mismatches 22; Indels 19; Gaps 1;
CC
CC QY 2 HKAYGFGAP-----KQQVTVAVYQEAAILACKPKTKVXSRLEWK 42
CC Db 235 YEALGWEAPVFGHMTLIINSATGKLSKRDSEVLQFIEQYRELVSQKPCSTSSLLGWS 294
CC
CC QY 43 KLGRSVSF 50
CC Db 295 PVGESEIF 302
CC
CC RESULT 5
CC GRETA_LACLA STANDARD; PRT; 156 AA.
CC ID GRETA_LACLA STANDARD; PRT; 156 AA.
CC AC Q9CHT2;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Transcription elongation factor greA (Transcript cleavage factor
CC greA).
CC DE GRETA OR LJ0636
CC GN Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
CC OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
CC OX NCBI_TaxID=1360;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=IL1403;
CC RX MEDLINE=21235186; PubMed=11337471;
CC RA Solotkin A., Winkler P., Mauger S., Jaillon O., Malarne K.,
CC Weissenbach J., Ehrlich S.D., Sorokin A.;
CC RA "The complete genome sequence of the lactic acid bacterium Lactococcus
CC lactis ssp. lactis IL1403."
CC RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: Necessary for efficient RNA polymerase transcription
CC elongation past template-encoded arresting sites. The arresting
CC sites in DNA have the property of trapping a certain fraction of
CC elongating RNA polymerases that pass through, resulting in locked
CC ternary complexes. Cleavage of the nascent transcript by cleavage
CC factors such as greA or greB allows the resumption of elongation
CC from the new 3' terminus. GreA releases sequences of 2 to 3
CC nucleotides (By similarity).
CC -!- SIMILARITY: Belongs to the greA/greB family.
CC -----
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CC -----
CC
CC DR EMBL; AE006296; AAK04734.1; -.
CC DR PIR; D86704; D86704.
CC DR HSSP; P21346; IGRJ.
CC DR HAMAP; MF_00105; -.
CC
```

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DR InterPro; IPR006359; GreA.
DR InterPro; IPR001437; GreA_GreB.
DR Pfam; PF01272; GreA_GreB; 1.
DR Pfam; PF03449; GreA_GreB_N; 1.
DR ProDom; PD004918; GreA_GreB; 1.
DR TIGRFAMs; TIGR01462; GreA; 1.
DR PROSITE; PS00829; GreA; 1.
DR PROSITE; PS00830; GreA; 2; FALSE_NEG.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 8 27 COILED COIL (POTENTIAL).
SQ SEQUENCE 156 AA; 17274 MW; 8558B8E3E02D4C88 CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 156;
Best Local Similarity 26.1%; Pred. No. 2.5;
Matches 24; Conservative 15; Mismatches 28; Indels 25; Gaps 4;

QY 3 KAYG-----FSAPKDDQ-----VVTAVYQEAIIACKTPKTKTVXSRLEWKILGR 46
Db 38 RSYGDLSENSEYEAADQAEIEGRISTVETMIRYAEIVDNAKIDKDEVA-----LGK 90

QY 47 SVSFVYVYQTLQGDGFK--NRAEMIDFNIRIKN 76
Db 91 NVTFEVGETDEESYQIVGTAEADPFSGKISN 122

RESULT 6
RUVB_BRUME STANDARD; PRT; 346 AA.
AC Q8YV5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holliday junction DNA helicase ruvB.
GN RUVB OR BWEI0334.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN SEQUENCE FROM N.A.
RP STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -!- SIMILARITY: Belongs to the ruvB family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE009475; AAL51515.1;
CC PIR; AH3293; AH3293.
CC HAMAP; MF 00016; -.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003959; AAA_ATPase_central.
CC InterPro; IPR004605; RuvB.
CC InterPro; IPR008823; RuvB_C.
CC InterPro; IPR008824; RuvB_N.
CC Pfam; PF00004; AAA; 1.

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DR Pfam; PF05491; RuvB_C; 1.
DR Pfam; PF05496; RuvB_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00635; ruvB; 1.
KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
KW Complete Proteome. 56 ATP (POTENTIAL).
FT NP_BIND 59 38240 MW; E6671088908197AC CRC64;
SQ SEQUENCE 346 AA; 38240 MW; E6671088908197AC CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 346;
Best Local Similarity 28.3%; Pred. No. 6;
Matches 17; Conservative 11; Mismatches 29; Indels 3; Gaps 2;

QY 4 AYGFSPKQDQVVAVYQEAAILACKTPKTVXSRLEWKKLGRSVSVFYVQOTLQGDF 61
DB 284 AAGLSEPRDAIEDIIBFYLIQGFLO-RTPRGRVLTAVAWQHLGLPAPAEIIQQSQYGLF 342

RESULT 8
TP2A-RAT STANDARD; PRT; 1526 AA.
AC P41516;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
GN TP2A OR TOP2 OR TOP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=3290677; PubMed=8390253;
RA Park S.H.; Yoon J.H.; Kwon Y.D.; Park S.D.;
RT "Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II."
RL Blochm. Biophys. Res. Commun. 193:787-793(1993).
CC -!- FUNCTION: Control of topological states of DNA by transient breakage and subsequent rejoining of DNA strands. Topoisomerase II makes double-strand breaks.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both negative and positive supercoils, whereas prokaryotic enzymes relax only negative supercoils.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.

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EMBL; Z46372; CAA86496.1; -
EMBL; Z19552; CAA79611.1; -
EMBL; Z29676; -; NOT_ANNOTATED_CDS.
DR HSSP; P06786; 1BGW.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003957; CBFA_NFYB_topis.
DR InterPro; IPR001241; DNA_topoisoi.
DR InterPro; IPR002205; DNA_topoisoi.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisoi; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR PRINTS; PR00615; COAATSUBUNTA.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD000742; DNA_topoisoi; 1.

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DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00433; TOP2C; 1.
DR SMART; SM00434; TOP4C; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
FT NP_BIND 159 164 ATP (POTENTIAL).
FT ACT_SITE 803 803 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1526 AA; 173220 MW; A1961ABDB1B050F CRC64;

Query Match 15.6%; Score 60.5; DB 1; Length 1526;
Best Local Similarity 27.2%; Pred. No. 30;
Matches 22; Conservative 12; Mismatches 22; Indels 25; Gaps 4;

QY 5 YGFSPKQDQVVAVYQEAAILACKTPKTVXSRLEW-----KKLGRSVSVFYV 53
DB 636 FKYSQPD-----DRAISLAFSKQVDDRKWLTFMEDRRQRKLLGLEPDIYLG 685

QY 54 QOTL---QGDFKNRAEMIDFN 71
DB 686 QTTMYLTYNDFINK-ELILFS 705

RESULT 9
CARB_BUCBP STANDARD; PRT; 1076 AA.
ID CARB_BUCBP
AC P59448;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
DE CARB OR BBP134.
GN Buchnera aphidicola (subsp. Baizhongia pistaciae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426901; PubMed=12522265;
RA Van Ham R.C.H.J.; Kamerbeek J.; Palacios C.; Rausell C.; Abascal F.; Bastolla U.; Fernandez J.M.; Jimenez I.; Postigo M.; Silva F.J.; Tamames J.; Viguera E.; Latorre A.; Valencia A.; Moran F.; Moya A.; "Reductive genome evolution in Buchnera aphidicola." Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
RL -!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.
CC -!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
CC -!- PATHWAY: Arginine biosynthesis.
CC -!- PATHWAY: Pyrimidine biosynthesis.
CC -!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
CC -!- SIMILARITY: Belongs to the carb family.

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EMBL; AE014016; AAO26868.1; -
DR HAMAP; MF_01210; -; 1.
DR InterPro; IPR006275; CarA_L_glu.
DR InterPro; IPR005483; CPase_L.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005480; CPase_L_D3.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR004362; MGS-like.
DR Pfam; PF00289; CPase_L_Chain; 2.
DR Pfam; PF02786; CPase_L_D2; 2.

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DR PFAM; PF02787; CPSase_L_D3; 1.
DR PFAM; PF02142; MGS; 1.
DR PRINTS; PRO0098; CPSASE
DR TIGRFAMs; TIGR01369; CPSaseII_lrg; 1.
DR PROSITE; PS00866; CPSASE_1; FALSE_NEG.
DR PROSITE; PS00867; CPSASE_2; 2.
KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW ATP-binding; Manganese; Complete proteome.
DR DOMAIN 1 403 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 404 553
DR DOMAIN 554 936
FT DOMAIN 937 1076
FT REPEAT 1 553
FT REPEAT 554 1076
FT NP_BIND 153 210
FT NP_BIND 303 354
FT METAL 285
FT METAL 286
FT METAL 288
FT METAL 289
FT METAL 301
FT METAL 301
FT METAL 829
FT METAL 841
SQ SEQUENCE 1076 AA; 120059 MW; 37PAF26E11AFEC03 CRC64;

Query Match 15.5%; Score 60; DB 1; Length 1076;
Best Local Similarity 30.2%; Pred. No. 24;
Matches 16; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 11 KQQQVTVAVXYQEAILACKTPKTKVXSRLEWKLGRSVFVYQOQLGDFKN 63
Db 688 KQPKNATVTNI-QEAILQAKSFKYPIIMIRPSVVGQSWEIVYDEKNTNFNN 740

RESULT 10
ID RUVB AGRT5 STANDARD; PRT; 346 AA.
AC Q8U9K6;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Holliday junction DNA helicase ruvbB.
GN RUVB OR AFU3722 OR AGR L 2225.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Woliam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).

CC -!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures
CC cruciform structure in supercoiled DNA with palindromic sequence,
CC indicating that it may promote strand exchange reactions in
CC homologous recombination. RuvAB is an helicase that mediates the
CC Holliday junction migration by localized denaturation and
CC reannealing (By similarity).
CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -!- SIMILARITY: Belongs to the ruvB family.
CC
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CC
CC EMBL; AF009303; AAL44532.1; -.
CC EMBL; AF008311; AAK89683.1; -.
CC PIR; A96270; A96270.
CC PIR; AF3014; AF3014.
CC HAMAP; MF_00016; 1.
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR003959; AAA ATPase_cent.
CC InterPro; IPR004605; RuvB.
CC InterPro; IPR008823; RuvB_C.
CC InterPro; IPR008824; RuvB_N.
CC Pfam; PF00004; AAA; 1.
CC Pfam; PF05491; RuvB_C; 1.
CC Pfam; PF05496; RuvB_N; 1.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMs; TIGR00635; ruvB; 1.
CC DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
CC Complete proteome.
CC NP_BIND 60 67 ATP (POTENTIAL).
CC SEQUENCE 346 AA; 38118 MW; 002E618EA234A189 CRC64;

Query Match 15.3%; Score 59.5; DB 1; Length 346;
Best Local Similarity 23.8%; Pred. No. 8;
Matches 15; Conservative 15; Mismatches 26; Indels 7; Gaps 3;

QY 4 AVGESAPKD--QQVTVAVXYQEAILACKTPKTKVXSRLEWKLKG----RSVSFVYQOQL 57
Db 285 AAGLSEPRDALEIIIEPYMIQQGFIQ-RTPRGRILITATAWKHLGLQPPKDLEAAQFRLL 343

QY 58 QGD 60
Db 344 EDD 346

RESULT 11
NRGI_CHICK STANDARD; PRT; 602 AA.
AC Q05199; O73750; O73751; O73752;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pro-neuregulin-1 precursor (Pro-NRGI) [Contains: Neuregulin-1
DE (Acetylcholine receptor inducing activity) (ARIA)].
OS NRGI OR ARIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX STRAIN=white leghorn; TISSUE=Brain;
RX MEDLINE=93201602; PubMed=8453670;
RX Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
RT "ARIA, a protein that stimulates acetylcholine receptor synthesis, is
RT a member of the neu ligand family."
RL Cell 72:801-815(1993).

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[2] SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).  
 RP TISSUE=Brain, and Spinal cord;  
 RC MEDLINE=98150951; PubMed=9491987;  
 RX Yang X., Kuo Y., Devay P., Yu C., Role L.;  
 RT "A cysteine-rich isoform of neuroligin controls the level of  
 RT expression of neuronal nicotinic receptor channels during  
 RT synaptogenesis.";  
 RL Neuron 20:255-270 (1998).  
 CC -!- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.  
 CC The multiple isoforms perform diverse functions: Cystine-rich  
 CC domain containing isoforms (isoforms 2-4) probably regulate the  
 CC expression of nicotinic acetylcholine receptors at developing  
 CC interneuronal synapses. The Ig-NRG isoform is required for the  
 CC initial induction and/or maintenance of the mature levels of  
 CC acetylcholine receptors at neuromuscular synapses.  
 CC -!- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a  
 CC proteolytically released soluble growth factor form. The membrane-  
 CC bound form does not seem to be active (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=ARIA, Ig-NRG;  
 CC IsoId=Q05199-1; Sequence=Q05199-1;  
 CC Note=Contains an Ig-like domain;  
 CC Name=2; Synonyms=CRD-NRG-BETA1A;  
 CC IsoId=Q05199-2; Sequence=VSP\_003445;  
 CC Note=The EGF-like domain is replaced by a Cysteine-rich domain  
 CC (CRD);  
 CC Name=3; Synonyms=CRD-NRG-BETA2A;  
 CC IsoId=Q05199-3; Sequence=VSP\_003446;  
 CC Note=The EGF-like domain is replaced by a Cysteine-rich domain  
 CC (CRD);  
 CC Name=4; Synonyms=CRD-NRG-BETA2B;  
 CC IsoId=Q05199-4; Sequence=VSP\_003445, VSP\_003446, VSP\_003447,  
 CC VSP\_003448;  
 CC Note=The EGF-like domain is replaced by a Cysteine-rich domain  
 CC (CRD);  
 CC -!- DEVELOPMENTAL STAGE: Isoforms 2-4 are detected at embryonic day 4  
 CC (ED4) in both visceral and somatic motor neurons of spinal cord  
 CC and is highest at ED6. Isoform 1 is not expressed until ED 6 in  
 CC spinal cord. At ED 11 both isoforms display comparable levels  
 CC -!- DOMAIN: The cytoplasmic domain may be involved in the regulation  
 CC of trafficking and proteolytic processing. Regulation of the  
 CC proteolytic processing involves initial intracellular domain  
 CC dimerization (By similarity).  
 CC -!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like  
 CC domain.  
 CC -!- PTM: Proteolytic cleavage close to the plasma membrane on the  
 CC external face leads to the release of the soluble growth factor  
 CC form.  
 CC -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Belongs to the neuroligin family.  
 CC -----  
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 CC -----  
 CC EMBL; L11264; AAA49037.1; --  
 CC EMBL; AF045654; AAC05670.1; --  
 CC EMBL; AF045655; AAC05671.1; --  
 CC EMBL; AF045656; AAC05672.1; --  
 CC PIR; A45769; A45769.  
 CC HSP; Q12784; IHRE.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR006210; IEGF.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/GJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1999).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH1183 SUBFAMILY.
DR PIR; J0507; HVMS39.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-Like; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 14.8%; Score 57.5; DB 1; Length 117;
Best Local Similarity 38.2%; Pred. No. 4.3;
Matches 13; Conservative 7; Mismatches 9; Indels 5; Gaps 2;

OY 29 KTKPKTKVXSLRW-KKLGRSVFVYQTLQGF 61
Db 58 QTPEK----RLEWVASISGGVSYTYYPDSVKGRF 87

RESULT 13
RVB RHET
ID RVB RHET STANDARD; PRT; 346 AA.
AC Q9L9C3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holliday junction DNA helicase ruvB.
GN RVB.
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE3;
RX MEDLINE=20156376; PubMed=10675620;
RA Martinez-Salazar J.M., Romero D.;
RT "Role of the ruvB gene in homologous and homeologous recombination in
Rhizobium etli.";
RL Gene 243.125-131(2000).
CC -1- FUNCTION: the ruvA-ruvB complex in the presence of ATP renatures
cruciform structure in supercoiled DNA with palindromic sequence,
indicating that it may promote strand exchange reactions in
homologous recombination. RuvAB is an helicase that mediates the
Holliday junction migration by localized denaturation and
reannealing (By similarity).
CC -1- SUBUNIT: Forms a complex with ruvA (By similarity).
CC -1- SIMILARITY: Belongs to the ruvB family.
CC
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CC
CC EMBL; U13645; AAA20987.2; -
CC HSSP; P24941; 1HCL.
CC WormPep; C05D10.2; CE29020.
CC InterPro; IPR003527; NAF kin.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.

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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF175525; AAF36814.1; -
CC HAMAP; MF_00016; -; 1.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR003959; AAA ATPase_cent.
DR InterPro; IPR004605; RuvB.
DR InterPro; IPR008823; RuvB_C.
DR InterPro; IPR008824; RuvB_N.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF05491; RuvB_C; 1.
DR Pfam; PF05496; RuvB_N; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00635; ruvB; 1.
KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase.
FT NP_BIND 60 67 ATP (POTENTIAL).
SQ SEQUENCE 346 AA; 38462 MW; 55EB3E4D3A273BEC CRC64;

Query Match 14.8%; Score 57.5; DB 1; Length 346;
Best Local Similarity 29.5%; Pred. No. 14;
Matches 13; Conservative 10; Mismatches 18; Indels 3; Gaps 2;

OY 4 AYGFSAFQD--QQVTAIXYQEAFLACKTPKTKVXSLRWKLG 45
Db 285 AAGLSEPRDAIEDIEPYMQQGFQ-RTPGRVLTATAWKHLG 327

RESULT 14
YPC2 CAEBL
ID YPC2 CAEBL STANDARD; PRT; 470 AA.
AC Q11179;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative serine/threonine-protein kinase C05D10.2 in chromosome III
(LOC 27.1.37).
GN C05D10.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du 2.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MAP
kinase subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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purposes requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; U13645; AAA20987.2; -
CC HSSP; P24941; 1HCL.
CC WormPep; C05D10.2; CE29020.
CC InterPro; IPR003527; NAF kin.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.

```

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DR SMART, SMO0220; S_TKC; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; transferase; Serine/threonine-protein kinase;
FT CHAIN 13 306 PROTEIN_KINASE.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 137 137 BY SIMILARITY.
SQ SEQUENCE 470 AA; 54038 MW; 8908849D15173DF0 CRC64;
Query Match 14.8%; Score 57.5; DB 1; Length 470;
Best Local Similarity 26.9%; Pred. No. 20;
Matches 21; Conservative 13; Mismatches 39; Indels 5; Gaps 2;
QY 3 KAYG-TSAPKDOQVAVXVQEAAILACKTPK----KTVXSRLEWKKLGRSVSVVYQQT 57
DB 75 KLYNIFRADNDRIYLAPEWEADLNHVIKGSILKDVHKQYIMCOLFAIRFLHSGNVL 134
QY 58 QGDFKRAEMIDFNIRIK 75
DB 135 HRDLKPSNVLLDADCRVK 152
RESULT 15
HA70_CLOBO STANDARD; PRT; 623 AA.
AC P46085;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hemagglutinin components HA-53 and HA-22/23 precursor.
GN HA-70 OR ANTP-70.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 7-29 AND 193-212.
RP STRAIN=Type C Stockholm / C-ST;
RX MEDLINE=95100958; PubMed=7802661;
RA Fujinaga Y., Inoue K., Shimazaki S., Tomochika K., Tsuzuki K.,
RA Fujii N., Waranabe T., Ohyama T., Takeshi K., Inoue K., Oguma K.;
RT "Molecular construction of Clostridium botulinum type C progenitor
RL toxin and its gene organization.";
RL Biochem. Biophys. Res. Commun. 205:1291-1298(1994).
[2]
SEQUENCE FROM N.A.
RP STRAIN=Type C Stockholm / C-ST / 468;
RX MEDLINE=94301293; PubMed=8028579;
RA Hauser D.F., Eklund M.W., Boquet P., Popoff M.R.;
RT "Organization of the botulinum neurotoxin C1 gene and its associated
RL non-toxic protein genes in Clostridium botulinum C 468.";
RL Mol. Genet. 243:631-640(1994).
CC -1- SUBUNIT: HA IS COMPOSED OF SUBCOMPONENTS HAVING 53, 33, 22-23, AND
CC 17 KDa. BOTULINUM TOXINS ARE PRODUCED AS PROGENITOR TOXINS OF
CC LARGE MOLECULAR SIZES OF 12S (M TOXIN), 16S (L TOXIN) AND 19S (LL
CC TOXIN). M TOXIN CONSISTS OF A NONTOXIC COMPONENT AND THE
CC NEUROTOXIN. L TOXIN CONSISTS OF THE M TOXIN AND HA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D38562; BAA07575.1; -
CC EMBL; S74768; AAB32849.1; -
CC EMBL; X72793; CAA51309.1; -
```

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DR InterPro; IPR003897; Clenterotox.
DR Pfam; PF03505; Clenterotox; 2.
DR PRINTS; PR01394; CLENTEROTOXN.
KW Hemagglutinin. 7 192 HEMAGGLUTININ COMPONENT HA-23A
FT CHAIN 10 192 (POTENTIAL).
FT CHAIN 13 192 HEMAGGLUTININ COMPONENT HA-23B
FT CHAIN 15 192 (POTENTIAL).
FT CHAIN 193 623 HEMAGGLUTININ COMPONENT HA-22A
FT CHAIN 193 623 HEMAGGLUTININ COMPONENT HA-22B
FT CHAIN 193 623 HEMAGGLUTININ COMPONENT HA-53.
SQ SEQUENCE 623 AA; 70649 MW; 115FBF1B2F3FB667 CRC64;
Query Match 14.8%; Score 57.5; DB 1; Length 623;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
QY 49 SFVYQQTLOGDFKRAEMIDFNIRIKN 76
DB 532 NYISYQLTIPGDFNNIASSI-FSPRTN 558
Search completed: July 15, 2004, 23:53:12
Job time : 4.25134 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 23:49:33 ; Search time 13.4118 Seconds  
(without alignments)  
1787.936 Million cell updates/sec

Title: US-09-852-797-76\_COPY\_23\_98

Perfect score: 388

Sequence: 1 YHKAYGFSAPKQQVTVAVX.....LQGFKNRAEMIDENIRIKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_invertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307.5	79.3	181	11 Q9CWD9	Q9cwd9 mus musculus
2	307.5	79.3	298	11 Q9J159	Q9j159 mus musculus
3	307.5	79.3	298	11 Q8CE95	Q8ce95 mus musculus
4	307.5	79.3	298	11 Q8CEK9	Q8cek9 mus musculus
5	80	20.6	309	4 Q96P11	Q96f11 homo sapien
6	80	20.6	310	4 Q9BX67	Q9bx67 mus musculus
7	80	20.6	355	4 Q8WNL8	Q8wvl8 homo sapien
8	74.5	19.2	310	11 Q9D8B7	Q9d8b7 mus musculus
9	74.5	19.2	310	11 Q9D1M9	Q9d1m9 mus musculus
10	74.5	19.2	310	11 Q9EPK4	Q9epk4 mus musculus
11	72.5	18.7	437	16 Q8E210	Q8e210 leptospira
12	71	18.3	300	13 Q7SYQ7	Q7syq7 xenopus lae
13	68	17.5	4440	5 Q8I5W6	Q8i5w6 plasmodium
14	67.5	17.4	641	17 Q970A5	Q970a5 sulfolobus
15	67	17.3	289	13 Q7ZW70	Q7zw70 xenopus lae
16	66	17.0	157	2 Q52245	Q52245 enterococcu

17	66	17.0	322	2 Q8L1C7	Q8llc7 enterococcu
18	65	16.8	275	15 Q8RVV7	Q8rvv7 thermoanaer
19	63.5	16.4	275	13 Q8AVV1	Q8avv1 xenopus lae
20	62.5	16.1	424	16 Q83E04	Q83ej4 coxiella bu
21	62.5	16.1	573	15 Q8DBY7	Q8db7 vibrio vuln
22	62	16.0	231	2 Q54941	Q54941 streptococc
23	62	16.0	374	16 Q8F2R9	Q8f2r9 leptospira
24	62	16.0	461	10 Q84RH9	Q84rh9 chlorarachn
25	60.5	15.6	188	16 Q8Z1O8	Q8z1o8 salmonella
26	60	15.5	124	16 Q92FV6	Q92fv6 rickettsia
27	60	15.5	214	16 Q7VR53	Q7vr53 candidatus
28	60	15.5	733	5 Q8SWD6	Q8swd6 encephalito
29	59.5	15.3	271	16 Q7VGU7	Q7vgu7 helicobacte
30	59.5	15.3	318	10 Q8LAY7	Q8lay7 arabidopsis
31	59.5	15.3	414	16 Q8UDV4	Q8udv4 agrobacteri
32	59.5	15.3	444	16 Q8Z7H5	Q8z7h5 salmonella
33	59.5	15.3	803	16 Q9ZJV3	Q9zjv3 helicobacte
34	59.5	15.3	1009	16 Q8XMB8	Q8xmb8 clostridium
35	59.5	15.3	1100	3 Q8X1U2	Q8x1u2 penicillium
36	59	15.2	255	2 Q848Y3	Q848y3 bacillus me
37	59	15.2	433	13 Q91859	Q91859 xenopus lae
38	59	15.2	438	11 Q9JLB7	Q9jlb7 mus musculu
39	59	15.2	510	11 Q9JLB8	Q9jlb8 mus musculu
40	59	15.2	549	11 Q9D006	Q9d006 mus musculu
41	59	15.2	549	11 Q9JLB9	Q9jlb9 mus musculu
42	59	15.2	551	5 Q94760	Q94760 strongyloce
43	58.5	15.1	301	16 Q92BC7	Q92bc7 listeria in
44	58.5	15.1	333	16 Q8YUV3	Q8yuv3 anabaena sp
45	58.5	15.1	491	5 Q8SVY4	Q8svy4 encephalito

ALIGNMENTS

RESULT 1				
Q9CWD9 PRELIMINARY; PRT; 181 AA.				
ID	Q9CWD9	PRELIMINARY;	PRT;	181 AA.
AC	Q9CWD9; (TREMELrel. 17, Last sequence update)			
DT	01-JUN-2001 (TREMELrel. 17, Last sequence update)			
DE	01-OCT-2003 (TREMELrel. 25, Last annotation update)			
DE	2410167M24Rik protein (Junction cell adhesion molecule 2).			
GN	JAM2 OR JCM2 OR 2410167M24RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;			
RX	MEDLINE=21085860; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,			
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzaletti J., Monbets P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

```

RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK010826; BAB27208.1; -.
DR EMBL; AK045095; BAC32219.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 181 AA; 20330 MW; 603B6114FEB11AEB CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 181;
Best Local Similarity 77.9%; Pred. No. 2e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YKXGFSAPKD-QQVTVAVYQAEAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOG 59
DB 23 YKANGFSASDKHQEVTVIEFQEAAILACKTPKTTSSRLWKVGQVSLVYQQALQG 82

QY 60 DFKRAEMIDFNIRKN 76
DB 83 DFKRAEMIDFNIRKN 99

RESULT 2
ID Q9JIS9 PRELIMINARY; PRT; 298 AA.
AC Q9JIS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion
DE molecule-3) (2410030G21Rik protein).
GN JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT the Immunoglobulin Superfamily, is Localized to Intercellular
RT Boundaries of Endothelial Cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Boraudo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hornmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordore P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyono-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AF255911; AAF81224.1; -.
DR EMBL; AJ291757; CAC20699.1; -.
DR EMBL; AK013914; BAB29053.1; -.
DR EMBL; AK010616; BAB27064.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 298;
Best Local Similarity 77.9%; Pred. No. 3.4e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YKXGFSAPKD-QQVTVAVYQAEAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOG 59
DB 23 YKANGFSASDKHQEVTVIEFQEAAILACKTPKTTSSRLWKVGQVSLVYQQALQG 82

QY 60 DFKRAEMIDFNIRKN 76
DB 83 DFKRAEMIDFNIRKN 99

RESULT 3
ID Q8CE95 PRELIMINARY; PRT; 298 AA.
AC Q8CE95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional cell adhesion molecule 2.
GN JAM2 OR JCAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028757; BAC26102.1; -.
DR MGD; MGI:1933820; Jam2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 33079 MW; CB8227EC13D349A3 CRC64;

Query Match 79.3%; Score 307.5; DB 11; Length 298;
Best Local Similarity 77.9%; Pred. No. 3.4e-30;
Matches 60; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 YKXGFSAPKD-QQVTVAVYQAEAILACKTPKTVXSRLEWKKLGRSVFVYQQTLOG 59

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DR EMBL; BC010690; AAH10690.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR KW Hypothetical protein; Immunoglobulin domain.  
FT NON\_TER 1  
SQ SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;  
  
Query Match 20.6%; Score 80; DB 4; Length 309;  
Best Local Similarity 32.0%; Pred.No.0.12;  
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps  
  
QY 21 YQEATLAC-KPKTKVXSRLEWKKL-GRSFVYVYQTLQGDFFKRAEMI 68  
DB 45 FSVSVLSGIITDSQTSDFRIEWKKIQDEQTYVFFDNKIKQGLAGRAIL 94  
  
RESULT 6  
Q9BX67 ID Q9BX67 PRELIMINARY; PRT; 310 AA.  
AC Q9BX67;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
DE Junctional adhesion molecule 3 precursor (Junctional adhesion  
DE molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein  
DE FLJ9288) (Hypothetical protein FLJ90828).  
DE JAM-2 OR JAM3.  
GN Homo sapiens (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
ID 1;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Cunningham S.A., Arrate M.P., Tran T.M.;  
RT "Cloning of Human Junctional Adhesion Molecule 3.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;  
RT "Heterogeneity of endothelial junctions is reflected by differential  
RT expression and specific subcellular localization of the three JAM  
RT family members.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;  
RT "Junctional adhesion molecules (JAMs) and interendothelial  
RT junctions.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Sachs U.J.H., Eva O., Berghoefter H., Santoso S.;  
RT "Characterization of Junctional Adhesion Molecule-3 on Human  
RT Platelets: A New Member of Immunoglobulin Superfamily.";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yanamoto J., Hakamatsu A., Nakamura Y., Kojima S., Nagahara K.,  
RA Masuho Y., Oho T., Okano K., Foshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RT "WEDO human cDNA sequencing project.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
DE EMBL; AF356518; AAK27221.1; -  
DE EMBL; AF344431; CSC69845.1; -  
DE EMBL; AF448478; AM20925.1; -  
DE EMBL; AK074769; BAC11195.1; -  
DE EMBL; AK075309; BAC111538.1; -

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DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; Ig; 2.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33EALDAB9 CRC64;

Query Match 20.6%; Score 80; DB 4; Length 310;
Best Local Similarity 32.0%; Pred. No. 0.12;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQDGFKNRAEMI 68
DB 46 FESVELSCIITDSQTSDFRIEWWKIQDEQTYVFFDNKIQDLAGRAEIL 95

RESULT 7
Q8WVL8 PRELIMINARY; PRT; 355 AA.
AC Q8WVL8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RA Hearn T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RN 2
RA Phillips H.M.;
RP SEQUENCE FROM N.A.
RT "Narrowing the critical region within liq24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during cardiogenesis."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro: IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.
SQ SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 20.6%; Score 80; DB 4; Length 355;
Best Local Similarity 32.0%; Pred. No. 0.14;
Matches 16; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 21 YQEAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQDGFKNRAEMI 68
DB 91 FESVELSCIITDSQTSDFRIEWWKIQDEQTYVFFDNKIQDLAGRAEIL 140

RESULT 8
Q9DBB7 PRELIMINARY; PRT; 310 AA.
AC Q9DBB7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23RIK protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S., Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 19.2%; Score 74.5; DB 11; Length 310;
Best Local Similarity 30.5%; Pred. No. 0.58;
Matches 18; Conservative 14; Mismatches 24; Indels 3; Gaps 3;

QY 21 YQEAILAC-KTPKTVXSRLEWKKL-GRSVSFVYQQTLQDGFKNRAEMI-DFNIRKN 76
DB 46 FESVELSCIITDSQTSDFRIEWWKIQDQTYVFFDNKIQDLAGRTDVFCKTSLRWN 104

RESULT 9
Q9DIM9 PRELIMINARY; PRT; 310 AA.
AC Q9DIM9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23RIK protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Borris A., Yoshida K., Haegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR ENBL; AK003326; BAB22715.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA43BD CRC64;

Query Match. 19.2%; Score 74.5; DB 11; Length 310;  
Best Local Similarity 30.5%; Pred.No.0.58;  
Matches 18; Conservative 14; Mismatches 24; Indels 3; Gaps 3;

Qy 21 YOBAILAC-KTPKKTVXSRLEWKKL-GRSVSFVYQQTLOGDFKNRAEMT-DFNIRIKN 76  
Db 46 FESVELSCITDTSQSPREIKWKLQDQQTYYVFDNKIQDLAGRTDVGKSLRIWN 104

RESULT 10  
Q9EPK4 PRELIMINARY; PRT; 310 AA.  
AC Q9EPK4  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Functional adhesion molecule-2, JAM-2 (1110002N23Rik protein)  
DE (Function cell adhesion molecule 3).  
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=11036763;  
RX Unimed=11036763;  
RT Aurrand-lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;  
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular  
RT Family?";  
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=121085660, PubMed=1217851;  
RA Kawai J., Shiragawa A., Shibata K., Yoshino M., Toch M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Scahill F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fleischer C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni I., Mashima J., Mazzarelli J., Nombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Borris A., Yoshida K., Haegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strausberg R.;



Page 7

	Matches	22: Conservative	12: Mismatches	32: Indels	9: Gaps	2:
QY	1	YHKAYGSAPKQQVTVAVYQERAILACKTPFKTVKSRLEWKLGRVSF-----VYV	53			
Db	540	HRTAYGTFIDYDEIVNRVF--AVKRIKPKITLISDNVVKARKVYFDDWVNAKVF	1			
QY	54	QQTIQGDFKNRAEMI	68			
Db	598	RETLPIGFDRRGPAI	612			

RESULT 15

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Q7ZWTO
ID Q7ZWTO PRELIMINARY; PRT; 289 AA.
AC Q7ZWTO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to junctional adhesion molecule 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RL Klein S., Strausberg R.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC046720; AAH46720.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_C2.
DR Pfam; PF00047; ig_2.
DR SMART; SM00409; IG2.
DR SMART; SM00408; IG2.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ SEQUENCE 289 AA; 31630 MW; 24354B5A37618945 CRC64;

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Query Match 17.3%; Score 67; DB 13; Length 289;  
Best Local Similarity 32.6%; Pred. No. 4.6;  
Matches 15; Conservative 8; Mismatches 21; Indels

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QY      22 QEAILACKTPKKTVXSRLEWKKLGR--SVSFVYYQQITLGDFKNRA   65
          :| | | | -| | | | : || | | | :|| | | |
Db      41 ESAELGCSYSSDFTSPRVEWKFNKDQETSFEFYDGSLTAPYKORA    86
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Search completed: July 15, 2004, 23:54:30  
Job time : 14.4118 secs

